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GenCore version 5.1.3
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OM protein - protein search, using sw model

March 10, 2003, 12:15:04 ; Search time 10.2637 Seconds (without alignments) 327.825 Million cell updates/sec Run on:

US-09-816-989A-1

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	outer membrane pro	hypothetical prote	Tola protein PA097	outer membrane int	histone H1 - sea u	histone H1-beta, e	probable zuotin [i	histone H1 - sea u	probable NLP/P60 f	DNA topoisomerase	hypothetical prote		membrane spanning	membrane spanning	DNA topoisomerase	histone H1-gamma,	kinetoplast-associ	histone H1 - Chlam	hypothetical prote	sperm tail-specifi	probable hupB - My	surface antigen A	hypothetical prote	histone H1-delta -	histone H1-II - Vo	, hypothetical prote	.O	histone H1, gonada	H1-1
SUMMARIES	ΩI	B43592	T03561	E83525	G64064	A25550	A28100	T50972	809388	T34625	JC6552	T34081	JV0057	F90725	G85576	G75403	A26721	A44937	859589	H96535	S51364	G70673	A60338	H59099	A32137	JN0748	T21503	A57591	HSURIP	JN0747
	DB	. 7	~	7	N	~	7	7	N	7	~						N	٦.	7	~	7	~	~	7	N	~	N	~	٦	7
	Length	384	461	347	372	210	211	445	206	277	1015	1130	421	394	394	1021	217	1052	231	318	1390	214	1528	101	185	241	335	621	248	261
dip	Query Match	50.6	48.5	45.8	44.6	43.4	43.1	42.5	42.2	42.2	42.2	42.2	41.9	40.4	40.4	40.4	40.1	40.1	39.8	39.8	σ	39.5	σ	39.2	38.9	38.6	38.6	8	38.0	38.0
	Score	84	80.5	92	74	72	71.5	70.5	70	70	70	70	69.5	67	67	67	66.5	99	99	99	99	65.5	65.5	65	64.5	64	64	63.5	63	63
	Result No.	-1	7	ო	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	hypothetical prote	probable erythrocy	histone H1 homolog	histone H1 (clone	penicillin-binding	histone H1 - rainb	histone H1 - midge	hypothetical prote	tolA protein [impo	zuotin-like protei	proton pump intera	penicillin-binding	translation initia	DNA topoisomerase	hypothetical prote
H96835	T49622	T09127	S61926	T06257	AD1683	HSTR1R	840436	T10644	AG0592	T39683	T08942	AD1311	A82298	B87553	829309
~	~	~	N	~	~	-	~	N	~	~	7	~	~	N	0
683	735	1701	182	288	826	206	244	266	376	442	628	827	868	899	217
38.0	38.0	38.0	37.7	37.7	37.7	37.3	37.3	37.3	37.3	37.3	37.3	37.3	37.3	37.3	37.0
63	63	63	62.5	62.5	62.5	62	62	62	62	62	62	62	62	62	61.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT

	B43592
	outer membrane protein TmpB - Treponema phagedenis
	C;Species: Treponema phagedenis
	C;Date: 30-Jan-1993 #sequence revision 12-Mar-1993 #text_change 08-Oct-1999
	C; Accession: B43592
	R;Yelton, D.B.; Limberger, R.J.; Curci, K.; Malinosky-Rummell, F.; Slivienski, L.; Schou
	Infect. Immun. 59, 3685-3693, 1991
	A; Title: Treponema phagedenis encodes and expresses homologs of the Treponema pallidum Tr
	A; Reference number: A43592; MUID:91372983; PMID:1894368
	A;Accession: B43592
	A;Status: preliminary
_	A; Molecule type: DNA
	A;Residues: 1-384 <yel></yel>
	A;Cross-references: GB:M58563; NID:9155066; PIDN:AAA27480.1; PID:9155067
	A; Note: the authors translated the codon TTC for residue 316 as Tyr, and CGA for residue
	C;Keywords: membrane protein

Gaps 7 Length 384; Indels 9 DB 2; Score 84; DB 2; Pred. No. 0.094; 5; Mismatches Query Match 50.6%; Best Local Similarity 64.9%; Matches 24; Conservative

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1 AKKYAKKEKAAK-KAYKKEAKAKAA-EAAAKEAAYEA 35 ద ò

RESULT 2

hypothetical protein - Rhodobacter capsulatus
CjSpecies: Rhodobacter capsulatus
CjSpecies: Rhodobacter capsulatus
CjSpecies: Rhodobacter capsulatus
CjAccession: 103561
Rjvlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A;Reference number: 214955; MUD:97404404; PMID:9256491
A;Reference number: 214955; MUD:97404404; PMID:9256491
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-461 <VLC>
A;Cross-references: BMBL:AF010496; NID:93128256; FIDN:AAC16214.1; FID:93128362
C;Genetics:
A;Map position: 1

Gaps ; 2; Length 461; Indels 8; Score 80.5; DB Pred. No. 0.25; 5; Mismatches Query Match
Best Local Similarity 60.0%;
Matches 21; Conservative ò

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30 AKEVVEKEAAAKDAAAKEAKAR-EEAAAKDAAAKA 63 1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35 g 7

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histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
C;Accession: A55550
R;Knowles, J.A.; Childs, G.J.
Nuccleic Acids Res. 14, 811.48133, 1986
A;Attle: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus anx A;Accession: A25550, MUID:87040778; PMID:3022245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cinces acrows acrows acrows acrows acrows and transcriptional patterns of the gene encoc Rilai, Z.C.; Childs, G. Mol. Cell. Biol. 8, 1842-1844, 1988
A,Title: Characterization of the structure and transcriptional patterns of the gene encoc A, Reference number: A28100, MuID:88246461; PMID:2837660
A,Rocession: A28100
A,Rocessio
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NiAlternate names: protein B24P7.270
CiSpecies: Neurospora crassa
CiDate: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
CiAccession: T50972
Rischulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000
A;Reference number: 225286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Species: Strongylocentrotus purpuratus (purple urchin)
C,Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 23-Feb-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A,Residues: 1-210 «XNO»
A,Cross-references: GB:X04488; NID:g9616; PIDN:CAA28177.1; PID:g9617
A,Cross-references: GB:X0408; NID:g9616; PIDN:CAA28177.1; PID:g9617
C,Superfamily: histore H1
C;Reywords: chromosomal protein; DNA binding; nucleosome; nucleus
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A;Cross-references: EMBL:AL389890; GSPDB:GN00116; NCSP:B24P7.270
A;Experimental source: BAC clone B24P7; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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66.7%; Pred. No. 1.2;
tive 2; Mismatches
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Matches 20; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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A; Introns: 98/3
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histone H1-beta,
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Outer membrane integrity protein.tolA - Haemophilus influenzae (strain RG KW20)

C;6gecies: Haemophilus influenzae

C;6gecies: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999

C;Accession: G64064; JC5212

R;Pleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, P. R;Pleischmann, R.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Killey, J.M.; Weidman, J.D.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gahem, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Residues: 1-372 - TIGR>

A;Residues: 1-372 - TIGR>

A;Cross-references: GB:U32722; GB:L42023; NID:G1573348; PIDN:AAC22041:1; PID:G1573353; T;Sen, K.; Sikkema, D.J.; Murphy, T.F.

Gene 178, 75-81, 1996

A;Reference number: JG5212; MUID:97080550; PMID:8921895

A;Accession: JC5212

A;Accession: JC5212

A;Accession: JC5212

A;Accession: JC5212

A;Accession: JC5212
                                                                                                                                                         C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83525
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reteus: preliminary
A;Reteus: preliminary
A;Reteus: a. 347 < s7TO>
A;Reteus: a. 347 < s7TO>
A;Residues: 1-347 < s7TO>
A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001
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A;Residues: 'V',2-47,'A',49-141,'R',143-164,'P',166-189,'R',191-202,'A',204-226,'A',228-
A;Cross-references: GB:U32470
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                                                                                                                          Fold protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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A;Note: the authors translated the codon CGT for residue 190 as Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 76; DB 2; Length 347;
Pred. No. 0.59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.8%;
ilarity 56.1%;
Conservative 5
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les 18; Conserv
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A,Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
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Length 1015;

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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002
C;Date: 07-Sep-1990 #sequences of the tola and tola genes and localization of their produc
A;Ttle: Nucleotide sequences of the tola and tola genes and localization of their produc
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosia-references: GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g148019
A;Experimental source: strain JM105
A;Experime
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A;Accession: JC6552
A;Molecule type: mRNA
A;Residues: 1-1015 <CZE>
A;Cross-references: GB:AF023910; GB:U63217; NID:g2642492; PIDN:AAC14193.1; PID:g2642493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein C02F12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34081
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Pred. No. 6.4;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U41545; PIDN:AAA83190.1; CESP:C02F12.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 KKEVKKEDTAKKDVKKEVKKETPKKTPAKRKAAESSSEESDF 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Riwiller, N. submitted to the EMBL Data Library, November 1995 submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid CO2F12. A;Reference number: 221473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----AKAKAAEAAKEAAY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70; DB 2;
Pred. No. 5.9;
6; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                              A,Gene: top1
C,Superfamily: eukaryotic type I DNA topoisomerase
C,Keywords: isomerase
F,974/Active site: Tyr #status predicted
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Best Local Similarity 42.9%;
Matches 18; Conservative
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Best Local Similarity 51.4%;
Matches 18; Conservative
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A; Residues: 1-1130 <MIL>
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DNA topoisomerase (EC 5.99.1.2) - slime mold (Physarum polycephalum)
NAlternate names: emega-protein; micking-closing enzyme; type I DNA topoisomerase
C.Species: Physarum polycephalum
C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C.Accession: JC652
C.Accession: JC652
C.Accession: JC652
C.Accession: JC652
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C.Accession: JC653
C.Accession: A.; Staron, K.
Gene 209, 39-44, 1998
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903188
histone H1 - sea urchin (Parechinus angulosus)
C;Species: Parechinus angulosus (angulate urchin)
C;Species: Parechinus angulosus (angulate urchin)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S03388
R;Hill, C.S.; Martin, S.R.; Thomas, J.O.
R;Hill, C.S.; Martin, S.R.; Thomas, J.O.
A;Title: A stable alpha-helical element in the carboxy-terminal domain of free and chrom A;Reference number: S09388; MUID:90060019; PMID:2583125
A;Accession: S09388
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                                                  Length 445;
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Pred. No. 1.6;
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                                                  DB 2;
                                                                                                                                                                                                                                                                                93 AAKOAKIDLAEAKKKAAEAKKKAEEAARKEAAERA 127
                                              Score 70.5; DE
Pred. No. 2.7;
4; Mismatches
                                                                                                                                                                                                                         2 KKYAKKEKAAKKAYKKEAKAKAA-EAAAKEAAYEA 35
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42.2%; Score 70; DB:
Best Local Similarity 54.3%; Pred. No. 2.1;
Matches 19; Conservative 1; Mismatches
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56.7%;
                                         42.5%;
ilarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Katus: preliminary
A; Molecule type: protein
A; Residues: 1-206 <HIL>
C; Superfamily: histone HI
C; Keywords: chromosomal protein
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                                         Query Match
Best Local Similarity
Matches 20; Conserv
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A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960; A;Experimental source: strain K-12, substrain MG1655 C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t C;Gene: tolA A;Gene: tolA A;Map position: 17 min
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A;Reaidues: 1-394 <STO>
A;Cross-references: GB:AE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:GN00145; UWGP:209
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC80774
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48.9%; Pred. No. 5.6;
tive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                        C; Keywords: nucleotide binding; P-loop; transmembrane protein F;14-14 /Domain: transmembrane #status predicted <MSS> F;78-301/Domain: helical #status predicted <HSR> F;78-362/Region: nucleotide-binding mottf A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 69.5; DB 2;
Pred. No. 3.2;
4; Mismatches 9;
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Pred. No. 5.6;
5; Mismatches E
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Best Local Similarity 52.6%;
Matches 20; Conservative
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Matches 22, Conservative
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Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: G85576
A;Status: preliminary
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                                                                                                                                                                                                                                                                A; Start codon: GTG
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DNA topoisomerase I - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accesion: 674603
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mal S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Szi Smith, H.O.; Venter, J.C.; Fraser, C.M.
Szience 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID: 20036896; PMID: 10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: DNA
A,Resdiques: 1.1021 «WHI.»
A,Scross-references: GB:AE001983; GB:AE000513; NID:g6459123; PIDN:AAF10943.1; PID:g645912'
A,Experimental source: strain R1
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40.4%; Score 67; DB 2; Length 1021;
Best Local Similarity 51.4%; Pred. No. 12;
Matches 18; Conservative 3; Mismatches 14; Indels
                                                                           167 AKKKAEAEAAKAAAEAQKKAEAAAAALKKKAEAAEAAAAAEAKKA 211
32
-----EAKAKAAEAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 1
C;Superfamily: bacterial type I DNA topoisomerase
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# GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

March 10, 2003, 12:15:01 ; Search time 7.97468 Seconds
 (without alignments)
182.035 Million cell updates/sec Run on:

US-09-816-989A-1 166 1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P29720 treponema p P50600 pseudomonas P4678 haemophilus P06144 mycobacteri P15869 strongyloce Q11102 caenorhabdi P19534 escherichia P40269 trypanosoma P40268 trypanosoma P40268 trypanosoma P40268 trypanosoma P5109 mycobacteri P5199 strongyloce Q99543 homo sapien Q08656 drosophila P51979 strongyloce P15870 strongyloce P51979 strongyloce P15870 strongyloce P15870 strongyloce P15870 strongyloce P51073 trypanosoma P40273 trypanosoma P40273 trypanosoma P40274 trypanosoma P40275 cherchinus Q08868 volvox cart P54103 mus musculu U74226 parchinus Q08864 volvox cart P40278 chironomus Q99500 stbrio chol P40276 chironomus Q94028 chironomus Q94026 glyptotendi
Σ	TWPB TREPH TOLA PSEAE TOLA PSEAE TOLA PSEAE TOLA PSEAE TOLA PSEAE TOLA PREIN HI LYPEI TOLA CAREL TOLA ECOLI HICE TRYCR HICE TRYCR ASR ENTCL HICE TRYCR HICE TRYCR HICE TRYCR ASR ENTCL HICE TRYCR ASR ENTCL HICE TRYCR HICE STRPU SPAĀ STRDO HID STRPU SPAĀ STRDO HID STRPU SPAĀ STRDO HID STRPU HID STRPU HID GUYBA HIL CHITE HIL CHITE HIL CHITE HIL CHITE HIL CHITE HIL GUYBA
DB	
Length	38 4 4 2 3 3 3 4 3 4 4 3 4 4 3 4 4 3 4 4 4 3 4
>-a	0.044444444444444444444444444444444444
Score	10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Result No.	1 1 2 6 4 5 9 7 8 6 0 1 1 1 1 1 1 2 1 2 1 2 1 1 1 1 1 1 1 1

## ALIGNMENTS

TRESULT 1  ID TMPB TREPH  ID TMPB TREPH  AC P297Z0;  AC P297S0;  DT 01-APR-1993 (Rel. 25, Created)  DT 01-APR-1993 (Rel. 25, Last sequence update)  DT 16-OCT-2001 (Rel. 40, Last annotation update)	ponemal membrane protein B. ponema phagedenis. teria; Spirochaetales; S L_TaxID=162;	SEQUENCE FROM N.A. STRAIN=KAZAIN 5; MEDLINE=91372983; PubMed=1894368; Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell F., Yelton D.B., Schouls L.M., van Embden J.D., Charon N.W.; "Treponema phagedenis encodes and expresses homologs of the Treponema palidum TmpA and TmpB proteins."; Infect. Immun. 59:3685-3693(1991)!- FUNCTION: TMP MAY SERVE AS A PORIN OR TRANSPORT PROTEIN FOR LARGE MOLECULES SUBCELLIJAR LOCATION: OUTHER MEMBRANE-ASSOCIATED.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SRIB outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).	EMBL; MS9563; AAA27480.1; PIR; B43592, BA3592. Antigen; Outer membrane; Repeat; Signal. SIGNAL 1 21 CHAIN 22 384 TREPONEMAL MEMBRANE PROTEIN B. CHAIN 151 235 17 X 5 AA TANDEM REPEATS OF K-A-A-[AKR] - REPEAT 151 155 1-1. REPEAT 156 160 1-2. REPEAT 161 165 1-3.	166 171 171 175 176 181 186 190 190 201 201 205 210 210 210 210 210 210 210 210 210 210
RESULT TMPB_TI ID TI AC PT DT DT OT DT	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	8	388888888	CC FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	
				<del></del>	· · · · · ·

Transport; Protein transport; Transmembrane; Repeat; Inner membrane;

EMBL; AE004530; AAG04360.1; -.

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STRAIN=ATCC 15692 / PAO1;

MEDLINE=20137377; PubMed=10984043;

MEDLINE=201377; PubMed=10984043;

Stover C.K., Pham F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., For B., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
  1-16.
1-17.
6 X 8 AA TANDEM REPEATS OF [EA]-A-A-R-X-
A-A-E.
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406:959-964(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOLA OR PA0971.
Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dennis J.J., Lafontaine B.R., Sokol P.A.,
                                                                                                                                                                                                                                                                                                                    Length 384;
                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                 6E94CBC74294DE8C CRC64;
                                                                                                                                                                                                                                                                                                            Score 84; DB 1;
Pred. No. 0.059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 AREMAAKEKAAKDKAAKEEAARKAAEEAARKAAEEA 254
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 AA
                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                         2-1.
2-2.
2-3.
2-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996)
                                                                                                                                                                                                                                                                 42677 MW;
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                                                                                                                                                                                                                                                                                                                                                                  24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS TO N-TERMINUS.
                                                                                                         243
252
261
270
279
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                                                                                                                                                                                                                                        288
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Best Local Similarity
                                                                                                                                                                                                                                                              384 AA;
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254
263
272
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIRE 4 / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Pritchman J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97080550; PubMed=8921895;
Sen K., Sikkema D.J., Murphy T.F.;
"Isolation and characterization of the Haemophilus influenzae tolQ,
tolR, tolA and tolB genes.";
Gene 178:75-81(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                               Score 76; DB 1; Length 347; Pred. No. 0.35;
                                                                                                                                                                                7; Indels
                                                                                                              347 AA; 37935 MW; EEDD4B04AA095945 CRC64;
                                                              POTENTIAL.
PERIPLASMIC (POTENTIAL)
                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                   1 AKKYAK---KEKAAKKAYKK---BAKAKAABAAKBAAYBA 35
                                                                                                                                                                                                                                                                                                                           TOLA HAEIN STANDARD; PRT; 372 AA. P44678; p94810; 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                5; Mismatches
                                                                                                                                                45.8%;
56.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, U32722, AAC22041.1; -. EMBL; U32470; AAC44596.1; -. HSSP; P19934; ITOL.
                                                                                                                                                                                 Conservative
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                                              16
37
347
216
                                                                                                                                                              Similarity
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                               Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                Tola protein.
TOLA OR HI0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rigR; HI0383;
                                                                                                                                                    Local Simi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=1479;
                                                               TRANSMEM
                                                                                                                                             Query Match
                                                                                                              SEQUENCE
                                                                             DOMAIN
                                              DOMAIN
                                                                                                                                                                                                                                                                                                            TOLA HAEIN
                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                RESULT 3
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DBH MYCSM
Q9ZHC5;
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SEQUENCE
  Query Match
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Matches
                                                                                                   RESULT 5
DBH MYCSM
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                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Lytechinus pictus (Painted sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; Nuclear protein; DNA-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Knowles J.A., Childs G.J.;
"Comparison of the late H1 histone genes of the sea urchins
"Comparison of the late H1 histone genes of the sea urchins
Lytechinus pictus and Strongelocentrotus purpuratus.";
Nucleic Acids Res. 14.8121-8133(1986).
-! FUNCTION: HISTONES H1 ARB NECESSARY FOR THE CONDENSATION OF
NUCLESOSME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                              AKAAAEAKAKA (IN STRAIN 1479).
A (IN STRAIN 1479).
F (IN STRAIN 1479).
                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                  44.6%; Score 74; DB 1; Length 372;
                                                                                                                                                                                                                                         8; Indels
                                                                                                                                              I -> V (IN STRAIN 1479).

N -> S (IN STRAIN 1479).

T -> A (IN STRAIN 1479).

S -> P (IN STRAIN 1479).

W, 266ECPOSCGC95544 CRC64;
                                                                 > P (IN STRAIN 1479).

> R (IN STRAIN 1479).

> A (IN STRAIN 1479).

> A (IN STRAIN 1479).
                                 SRIPLASMIC (POTENTIAL).
-> A (IN STRAIN 1479).
-> R (IN STRAIN 1479).
           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                           5 AKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; LinkerhIst N.
Pfam; PP00538; linker histone; I.
ProDom; PD000373; Linkerhist N; I.
                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Embryo;
MEDLINE=87040778; PubMed=3022245;
                                                                                                                                                                                            39831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X04488; CAA28177.1; -.
PIR; A25550; A25550.
                                                                                                                                                                                                                            58.1%;
                                                                                                                                                                                                                                        18; Conservative
                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00526; H15; 1.
                                                       142
1165
1165
223
233
234
249
254
330
330
                                                                                                                                                                               333 3
372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 AA;
                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
 Complete proteome DOMAIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7653;
                                                                                                                                                                                                                                                                                                                                                                                                     Late histone Hl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosomal
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ytechinus.
                                                                                                                                                                               VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                           H1 LYTPI
P06144;
                      PRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOI. Gen. Genet. 260:475-479(1998).

-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee B.H., Murugasu-Oei B., Dick T.; "Upregulation of a histone-like protein in dormant Mycobacterium
                                                        4
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                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp)
HUP OR HLP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00045; HISTONE LIKE; 1.
DNA-Dinding; DNA condensation; Repeat.
DOMAIN 1 90 BACTERIAL HISTONE-LIKE DOMAIN.
NOMAIN 101 205 DEGENERATE REPEATS REGION.
  DB 1; Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21230 MW; CASF577F61F7EF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                     9
                                                                                                                                          157 AKKAAKKPAAKKPAKKPAKKAAKKAAKKAAKAA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKK---EKAAKK-AYKKEAKAKAAEAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
43.4%; Score 72; DB 1; 59.0%; Pred. No. 0.57; ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAAKKAYKKEA-KAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                  208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 700084 / mc(2)155;
MEDLINE-99110209; Pubmed-9984918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00216; Bac DNA bInding; 1.
ProDom; PD000945; Bac DNAbind; 1.
SMART; SM00411; BHL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interPro; IPR000119; Bac_DNAbind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seque
15-JUL-1999 (Rel. 38, Last annot
Histone H1-beta, late embryonic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF068138; AAD13809.1; -. HSSP; P02346; 1HUU.
                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21, Conservative
                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 AA;
                         Local Similarity
tes 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
H1B STRPU
ID H1B STRPU
AC P15869;
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EMBL; U41545; AAK39135.1; -.
WormPep; C02F12.7; CE03901.
Hypothetical protein; Coiled coil.
DOMAIN 121
DOMAIN 805 1061 COILE (POTENTIAL).
SEQUENCE 1130 AA; 131485 MW; BOFDZEFE3D99FB09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriol. 171:6600-6609(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90078104; PubMed=2687247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91296736; PubMed=2068069;
                                                                                                                                                                                                                                   42.2%;
                                                                                                                                                                                                                                                          ilarity 51.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH PORINS
                                                                                                                                                                                                                                                     Local Similarity
es 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOLA ECOLI
P19934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K12;
                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
TOLA_ECOLI
                                                                                                                                                                                                                                                                                          Matches
        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilb.sib.ch).
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                             MEDLINE=88246461; PubMed=2837660;
Lai Z.-C., Childs G.;
"Characterization of the structure and transcriptional patterns of
the gene encoding the late histone subtype H1-beta of the sea urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 211 AA; 22169 MW; 9F214581334BBE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä
                                                                                                                                                                                                                                                                                                            Strongylocentrotus purpuratus.";
Mol. Cell. Biol. 8:1842-1844(1988).
--- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION (NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
---- SUBCELLULAR LOCATION: Nuclear.
--- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.1%; Score 71.5; DB 1; Length 211; 66.7%; Pred. No. 0.65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miller N.; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 131.5 kba protein C02F12.7 in chromosome X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 АККААКК-РААККААККУАККРААККААКК 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKE 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist N.
Pfam; PP00538; linker histone; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000373; Linkerhist N; 1. SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: WEAK, TO MYOSINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M20314; AAA30052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A28100; A28100.
                                                                                 Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02259; 1HST
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                    NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
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YL17 CABEL

D. VL17 CABEL

AC 011102;
DT 01-NOV-1997
DT 16-OCT-2001

DE Hypothetical
GN CO2F12.7.

OS Caenorhabdit
OC Bukaryota; M
OC Bukaryota; M
OC RABABLICAELS

OC RABABLICAELS

OC RABABLICAELS

OC RABABLICAELS

OC RESULT TAXID=6

RN [1]

RP SEQUENCE FRO

RP SEQUENCE FRO

RR STRAIN=BRIST

RA MILLER N.;
CC ------------

CC This SWISS-F

CC the European

CC use by non

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CC wentities rec

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CC rection and cC re
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                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97061202; PubMed=8905232;
Oshlma T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STROMAINSALD '/ MG4655;
STRAMBSALD '/ MG4655;
BEDALINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Rirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97133271; PubMed=8978668;
Derouiche R., Gavioli M., Benedetti H., Prilipov A., Lazdunski C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Levengood S.K., Beyer W.F. Jr., Webster R.E.; membrane protein involved in colicin uptake contains an extended helical region."; membraned helical region."; Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Bscherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yano M., Horiuchi T.;
M.A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
                                                                           9
Score 70; DB 1; Length 1130;
Pred. No. 3.7;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                        421 AA
                                                                                                                                               6 KKEKAAKKAYKKEAKAKA-----AEAAKEAAYE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tola protein.
TOLA OR CIM OR EXCC OR LKY OR B0739.
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Acid shock protein precursor.
                                                                                                                                                                                                     Local Similarity
les 20; Conserv
                                                                                                                                                                                                                                                                                                                                              TRYCR
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Matches
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ASR ENTCL
                                                                                                                                                                                                                                                                                                                     RESULT 10
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                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypanosoma cruzi.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                        OF BACTERIOPHAGE DNA.
SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ecodene, EG11007, tolA.
Transport, Protein transport, Bacteriocin transport, Transmembrane,
                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                             Lubkowski J., Hennecke F., Plucckthun A., Wlodawer A.;
"Filamentous phage infection: crystal structure of g3p in complex
with its coreceptor, the C-terminal domain of TolA.";
Structure 7:711-722 (1999).
-!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A
COLICINS (COLICINS A, E1, E2, E3, AND K). NECESSARY FOR THE
COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL
BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95059220; PubMed=7969272;
Aaslund L., Carlsson L., Henriksson J., Rydaaker M., Toro G.C.,
Galanti N., Pettersson U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
        "TolA central domain interacts with Escherichia coli porins."; EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69.5; DB 1; Length 421; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A gene family encoding heterogeneous histone H1 proteins in Trypanosoma cruzi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8B2F52B4B97C655E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; Inner membrane; 3D-structure; Complete proteon DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
TRANSMEM 14 34 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERIPLASMIC (POTENTIAL)
                                                    X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421
MEDLINE=99332679; PubMed=10404600;
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ز
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HICG_TRYCR STANDARD; PRT; 87 AA. P40259; P40271; 01-FRB-1995 (Rel. 31, Created) 1. PFB-1995 (Rel. 31, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) Histone HI.C6/HI.C9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KYAKKEKAAKKA-----YKKEAKAKAAEAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Biochem. Parasitol. 65:317-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AE000177; AAC73833.1; -. EMBL, D90713; BAA35405.1; -. PIR; JV0057; JV0057. PDR; 1TOL; 20-MAY-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 AA; 43156 MW;
                                                                                                                                                                                                                                                                                                                                                                       EMBL; M28232; AAA24683.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                       AND LAMB
Lloubes R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                             Chromosomal protein; Nuclear protein; DNA-binding; Multigene family SEQUENCE 87 AA; 9005 MW; 843FF90F5F73922D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Thlahuen 2;
MEDLINE=9505520; PubMed=7969272;
Aaslund L., Carlsson L., Henriksson J., Rydaaker M., Toro G.C.,
Galanti N., Pettersson U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
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                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       41.3%; Score 68.5; DB ilarity 52.6%; Pred. No. 0.62; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma cruzi.";
Mol. Biochem. Parasitol. 65:317-330(1994).
                                                                                                                                                                                                                                                              EMBL; L27120; AAA66479.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L27115; AAA66478.1; -.
                                                                                                                                                                                                                                                                                                  EMBL; L27117; AAA66481.1; -.
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les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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us-09-816-989a-1.open.rsp

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InterPro, IPR001386; Histone H1/H5.
InterPro, IPR002136; Linkerhist. N.
Pram, PR00538; linker histone; J.
ProDom, PD000373; Linkerhist. N. 1.
SMART, SMO826; H15, 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 217 AA; 22658 MW; C7251EED3413B185 CRC64;
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC:13192; ZRF1.
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                          Similarity
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  HSSP; P02259; 1HST
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxiD=9606;
                                                                                                                           Query Match
Best Local Simi
Matches 20;
                                                                                                                                                                                                                                                                                 ZRF1 HUMAN
Q99543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                       ZRF1 HUMAN
                                                                                                                                                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDIANE-3031476; MEDLINE-87172742; Pubmed-3031476; Knowles J.A., Lai Z.-C., Childs G.J.; Medlation, characterization, and expression of the gene encoding the late histone subtype H1-gamma of the sea urchin Strongylocentrotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strongylocentrotto, purpuratus (Purple sea urchin).
Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i - FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-i - SUBCELLULAR LOCATION: Nuclear.
-i - SIMILARITY: BELONGS TO THE HISTONE HI/HS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                              Seputiene V., Motiejunas D., Suziedelis K., Suziedeliene E., "Molecular characterization of acid-inducible Asr protein of
                                                                                                                                                                                                                                                                                                                                                                                             41.3%; Score 68.5; DB 1; Length 101; 52.8%; Pred. No. 0.7; tive 5; Mismatches 7; Indels 9
                                                                                                                        Escherichia coli.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ASR FAMILY.
                                                                                                                                                                                                                                                                                                                                                    22 101 ACID SHOCK PROTEIN.
101 AA; 10254 MW; 0FAF9D6EED61D26E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KKYAK----KEKAAKKAYKKEAKAKAAEAAKEAA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 AA
                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                              EMBL; AF405542; AAK92015.1; ALT INIT.
InterPro; IPR000104; Antifreeze_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell. Biol. 7:478-485(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M16033; AAA30059.1; -. PIR; A26721; A26721.
                                                                                                                                                                                                                                                                                                                                                                                                                        19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histone H1-gamma, late.
              Enterobacter cloacae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                 SEQUENCE FROM N.A.
                                                       NCBI_TaxID=550;
                                        Enterobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           purpuratus."
Mol. Cell. B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIG STRPU
P07796;
                                                                                                                                                                                                                                                                                                                          Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
HIG_STRPU
a
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                                                                     ä
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Westendorf J.M.; "Identification of novel M phase phosphoproteins by expression
40.1%; Score 66.5; DB 1; Length 217; 50.0%; Pred. No. 2.1; tive 3; Mismatches 8; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97039687; PubMed=8885239;
Matsumoto-Taniura N., Pirollet F., Monroe R., Gerace L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32F269B4A532AD46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Zuotin related factor-1 (M-phase phosphoprotein 11)
ZRF1 OR DNAJC2 OR MPHOSPH11 OR MPP11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Nuclear (By similarity).
-i- PTM: PHOSPHORYLAGTED IN (MITOTIC) PHASE.
-i- SIMILARITY: CONTAINS 1 J DOMAIN.
-i- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
                                                                                                                                                                          1 AKKYAKKEKAAKKAYK-----KEAKAKAABAAKEA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaperone, Nuclear protein, Phosphorylation.
DOMAIN 94 163 J-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.1%; Score 66.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIN; 605502; -
InterPro; IPR001623; DnaJ N.
InterPro; IPR001005; Myb DNA_binding.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00249; myb DNA_binding; 2.
SMART; SM00271; DnaJ; 1.
SMART; SM00395; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00037; MYB_1; PALSE_NEG.
PROSITE; PS00034; MYB_2; 1.
PROSITE; PS50090; MYB_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X98260; CAA66913.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Biol. Cell 7:1455-1469(1996).
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SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                   Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-1997) to the SWISS-PROT data bank.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILIZE IT, AND PREYENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY)
  JNA-binding protein HU homolog (Histone-like protein) (Hlp) (21-kDa
                                                                                                                                                                                                                       MEDLINE=9829587; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd 'Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prasad H.K., Annapurna P.S., Dey A.B., Tyagi J.S., Jain N.K.,
                          laminin-2-binding protein).
HUP OR HLP OR LBP21 OR RV2986C OR MT3064 OR MTCY349.01.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 71-86, AND DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000119; Bac DNAbind.
InterPro; IPR001386; Histone H1/H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00216; Bac_DNA_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00624; HĪSTONEHS.
ProDom; PD000945; Bac DNAbind; 1.
SMART; SM00411; BHL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 UE
22187 MW;
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Best Local Similarity 52.4%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AE007127, AAK47393.1;
HSSP, P02346; 1HUU.
TIGR; MT3064; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z83018; CAB05427.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuberculist; Rv2986c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 AA;
                                                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bishai W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Savita P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long a sits content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DERMYLLIDS.

DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.

POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT

STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Perrygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.8%; Score 66; DB 1; Length 1391; 48.7%; Pred. No. 11; tive 1; Mismatches 9; Indels
                       10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         694
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                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
10-FEB-1995 (Rel. 31, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Axoneme_associated protein mst101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      656, KKLAKKEKETAEKKKCEKAAKKRKEAAEKKKCAEAAKKE
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(Rel. 38, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                               - 281 KKFKEEEKAKKEAEKKAKAEAKRKEQEAKEKQRQA 315
48.6%; Pred. No. 4.7; ive 7; Mismatches
                                                                     2 KKYAKKEKAAKKAYKK-EAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                   PRT; 1391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0020733; Dhyd\mst101(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95045538; PubMed=7957199;
                                                                                                                                                                                                                                                                                                                                                                  MST101(2).
Drosophila hydei (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X73481; CAA51876.1; -
                     17; Conservative
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                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S34154; S34154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
tes 19; Conserv
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999
15-JUL-1999
16-OCT-2001
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                                                                                                                                                                                                                               DROHY
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P95109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
  Best Local
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DOMAIN
                                                                                                                                                                               RESULT 14

MST2_DROHY
IN TAT2_DROHY
IN TAT2_DROHY
IN TO 11-FE
DT 01-FE
DT 01-FE
DT 01-FE
DT 16-OC
OC Entex
OC E
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ID DBH M
AC P9510
DT 15-JU
DT 15-JU
                       Matches
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S.L.,

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                                                                                                                                                                                      ong as its content is in no way loved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65.5; DB 1; Length 214;
Pred. No. 2.6;
3; Mismatches 10; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Repeat; Complete proteome.
DOMAIN 1 90
BACTERIAL HISTONE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEGENERATE REPEATS REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB09AF20FB353544 CRC64;
                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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Search completed: March 10, 2003, 12:17:07 Job time : 8.97468 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

March 10, 2003, 12:15:01 ; Search time 18.5338 Seconds
 (without alignments)
 389.109 Million cell updates/sec

US-09-816-989A-1 166 Title: Perfect score:

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp\_archea:\* sp\_bacteria:\* SPTREMBL •• Database

sp\_fungi: sp\_human:\* sp\_invertebrate:\* sp\_mammal:\* sp\_mhc:\* sp\_organelle:\* sp\_unclassified:\* sp\_vertebrate:\* sp\_bacteriap:\* sp\_rodent:\* sp\_virus:\* sp\_plant:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp archeap:\*

# SUMMARIES

COLUMNIA	_		Description		29WWX1 Q9wwx1 pseudomonas	068124 rhodobacter	98WQ44 leishmania	Q8t9r3 1	001395		Q9BMY8 Q9bmy8 leishmania		Q9P3Q8 neurospora		4705 physarum po	995un5		5UN6 095un6 trypanosoma	5vvx60	001100
			B ID	1 1 1	2 09	2 06	5 08	5 08	2 00	2 09	5 09	16 0	3	16 0	2	5 09	2	5	5	6
		Query	Length D	1 1 1 1 1 1 1	372	461	86	111	275	395	101	244	445	277	1015	78	741	83	112	000
	ф	Query	Match		48.8	48.5	47.9	47.9	46.4	46.4	45.5	45.2	42.5	42.2	42.2	41.9	41.6	41.3	41.3	,
			Score		81	80.5	79.5	79.5	77	77	75.5	75	70.5	70	70	69.5	69	68.5	68.5	000
		Result	No.		-1	7	m	4	S	9	7	ω	თ	10	11	12	13	14	15	71

Q17321 chironomus	Q9agv7 corynebacte	Q98fb4 rhizobium l	Q9nfp6 trypanosoma	Q8x965 escherichia	Q9vbl3 drosophila	Q9rul0 deinococcus	Q9nfj8 trypanosoma	Q9n6j8 trypanosoma	Q9nfj4 trypanosoma				O60414 homo sapien		Q26938 trypanosoma	Q90zd7 bufo bufo g	Q39576 chlamydomon		Q91p19 arabidopsis	Q8xwi3 ralstonia s	Q9vwk3 drosophila	Q9xhe2 chlamydomon	Q9x342 bacillus an	Q9vfh1 drosophila	Q45302 corynebacte	Q9ant7 brevibacter	Q8suw1 encephalito	O46142 mytilus edu
017321	Q9AGV7	Q98FB4	Q9NFP6	Q8X965	Q9VBL3	Q9RUL0	Q9NFJ8	819N6Q	Q9NFJ4	679N6D	Q9NFJ9	060415	060414	6IQN6Ö	Q26938	Q90ZD7	039576	Q8VWK4	Q9LPL9	Q8XWI3	Q9VWK3	Q9XHE2	Q9X342	Q9VFH1	Q45302	Q9ANT7	QBSUW1	046142
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41	41	41	40	40	40	40.4	40	40	40.1	40	40.1	40.1	40.1	40.1	40.1	39	39	39	39	39	39	39	39	39	39	39	39	38
68	68	69	67.5	67	29	67	66.5	66.5	66.5	66.5	66.5	66.5	66.5	66.5	99	99	99	99	99	65.5	65.5	65.5	65	65	65	65	65	64.5
11	18	19	20	21	22	23	24	52	56	27	58	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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STRAIN=MT-2;
MEDLINE=96198174; PubMed=8626299;
Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.;
Rodriguez-Herva J.J., Pappidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96422022; PubMed=8824639;
Rodriguez-Herva J.J., Ramos J.;
"Characterization of an OprL null mutant of Pseudomonas putida.";
J. Bacteriol. 178:5836-5840(1996).
                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MT-2;
Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                   372 AA.
                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell envelope.";
J. Bacteriol. 178:1699-1706(1996)
                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MT-2;
Rodriguez-Herva J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                   Tola protein.
                                                                           Q9WWX1
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RESULT 1
                                             XMM60
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8888

RESULT 2

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Eukaryota; Metazoa; Arthropóa; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 X 16 AA APPROXIMATE TANDEM REPEATS OF X-{KQ]]-K-C-{AE}-E-X-A-{X}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Papageorgiou F., Soteriadou K.;
"Identification of a Leishmania infantum gene encoding for an histone
                                                                                                                                                                                                                                                                                                                                                           Leishmania infantum.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
47.9%; Score 79.5; DB 5; Length 111;
Best Local Similarity 67.6%; Pred. No. 0.09;
Matches 23; Conservative 3; Mismatches 5; Indels
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Pred. No. 0.42;
3; Mismatches 12; Indels
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H1-like nuclear protein.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AF469106; AAL76335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-i- TISSUB SPECIFICITY: TESTIS (BY SIMILARITY).
-i- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 AA; 11162 MW; 16168F3B54960E83 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
Axoneme-associated protein MST101(3).
MST101(3) OR DMMST101.
Drosophila hydei (Fruit fly).
                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                  111 AA
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                                    1 AKKYAKK--EKAAKKAYKKEAKAKAAEAAKEAA
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FlyBase; FBGT0020732; Dhyd\mst101(3).
Sperm; Repeat; Multigene family.
DOMAIN
                                                                                                                                                                                                                                                     Created)
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01-JUL-1997 (TrEMBLrel. 04, Created)
                                                                                                                                                                                               PRT;
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57.1%;
                                                                                                                                                                                                                         Q8T9R3;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tzortzakis N., Papageorgiou F.T., Tzinia A.K., Soteriadou K.P.; "Identification and characterization of a novel Leishmania gene encoding for a putative histone H1- like transcription factor."; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AJ237814; CAD21431.1; -. Nuclear protein SQUENCE 98 AA, 9999 MW; 0A4AB93089D6C261 CRC64;
                                                                                                                                                                                               9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SE1003;
MEDLINE=97404404; PubMed=9256491;
MEDLINE=97404404; PubMed=9256491;
Vlcek C., Pacces V., Maltsev N., Pacces J., Haselkorn R., Fonstei Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003.";
Proc. Natl. Acad. Sci. U.S. A. 94:9384-9388(1997).
EMBL; AF010496; AAC16214.1; --
Hypothetical procein.
SEQUENCE 461 AA; 49516 MW; DD8DA03418BC0368 CRC64;
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Pred. No. 0.08;
3; Mismatches 5; Indels
                                                                                                                                       Length 372;
                                                                                                                                                                                               9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                 40133 MW; 87F49785ECC3C0BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) Hypothetical 49.5 kDa protein.
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Last annotation update)
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                                                                                                                                                                                                                                                     1 AKKYA-----KKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35
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                                                                                                                                       / Match 48.8%; Score 81; DB 2; Local Similarity 56.1%; Pred. No. 0.21; hes 23; Conservative 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               461 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                         InterPro; IPR001386; Histone HI/H5. PRINTS; PR00624; HISTONEH5. SEQUENCE 372 AA; 40133 MW; 87F4!
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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EMBL; X74218; CAB50780.1; -.
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Matches ( 23; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhodobacter
                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                      Best Loca
Matches
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Matches

RESULT 3

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2,

3; Gaps

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Gaps

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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Thomson N.R. Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Rabbinowitsch E., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                              Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Complete genome sequence of the model actinomycete Streptomyces
                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL513407; CAC28545.1; -.
SEQUENCE 244 AA; 25524 MW; 61999D62CA23A7B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 75; DB 16
Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AKKEKAAKKAYKKEA----KAKAAEAAKEAAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.1%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 45.2%;
1 Similarity 61.8%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5141;
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                                                                                            NCBI_TaxID=1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Q9P3Q8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
Q9XAQ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5659;
                                                                                                                                                                                                                                                                                                                                          Erwinia chrysanthemi.
Bacteria; Proteobacteria; gamma subdívision; Enterobacteriaceae;
Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ray M.C., Vianney A., Cotte-pattat N., Lazzaroni J.;
"characterization of the Erwinia chrysanthemi tol-pal genes.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ297885, CAS2708.1; -.
SEQUENCE 395 AA, 41601 MW; 3COCIDC12E181013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melo G.S., Fragoso S.P., Fasel N.S., Mendonca S.C.F.; "Cloning and sequencing of histone H1 gene from Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.4%; Score 77; DB 2; Length 395;
51.2%; Pred. No. 0.61;
iive 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF287632; AAG66089.1; -.
Interpro; IPR001386; Histone H1/H5.
PRINTS; PR00624; HISTONEH5.
SEQUENCE 101 AA; 10078 MW; 3D3AE865FD9B6846 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 AKKKAEBERAKAKAAADAKOKAEBEAKAKAABAAKEKAAADA 240
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45.5%; Score 75.5; DB 5;
Best Local Similarity 55.3%; Pred. No. 0.23;
Matches 21; Conservative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 AKKPAKKAGAKKAAKRLAKKAAPKKAAKKAAKKPAKKA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKK---EKAAKKAYKKEAKAKAAEAAKEAAYEA
                                                                                                                          395 AA
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                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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01-JUN-2001 (TrEMBLrel. 17, C
01-JUN-2002 (TrEMBLrel. 21, L
01-JUN-8002 (TrEMBLrel. 21, L
Putative secreted protein.
SCO1805 OR SCI33.04.
                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel: 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 51.2
nes 21; Conservative
                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leishmania amazonensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amazonensis.";
                                                                                                                                                                                                                                                                              TolA protein.
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                                                                                                                   Q937K4
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Q9BMY8
AC Q9BMY8
AC Q9BMY 01-J7
DT 01-J
                                                    RESULT 6
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Gaps

4.

Indels

7;

34

DB 16; Length 244;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                           Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 70.5; DB 3; Length 445;
Pred. No. 3.6;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 German Neurospora genome project;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL389890; CAB97292.1; -.
HASP, P25685; 1HDJ.
INTEPRO; IRROUGE3; DNaJ.N.
Pfam; PF00226; DNaJ; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS00076; DNaJ 1; UNKNOWN_1.
PROSITE; PS00076; DNAJ 2; 1.
SRQUENCE 445 AA; 50612 MW; 982B97EFAZDA34E6 CRC64;
                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 KKRLEKEAAEKKAAEEAAKKAAEEAAAKEAEEKA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KKYAKKEKAAKKAYKKEAKAKAA-EAAAKEAAYEA 35
86 AKKEAAAKKATAKKATAEKKAAAEKAAAKRAAKE 119
                                                                                                                                                                                                      Created)
                                                                                                                                             PRT;
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1;

Gaps

10;

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Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porto R.M., Amino R., Elias M.C.Q., Faria M.B., Schenkman S.; "Histone H1 is phosphorylated in non-replicating and infective forms of Trypanosoma crual."; Submitted (JuL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AV046274; AAL02283.1; -. NON TER 78
                                      MEDLINE=98245940; PubMed=9583949;
Czerwinski R.M., Lipniacki A., Staron K.;
"CDNA cloning of Physarum polycephalum DNA topoisomerase I and
                                                                                                                                                                                                                                                                                                                                                   Score 70; DB 5; Length 1015;
Pred. No. 9.3;
6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.9%; Score 69.5; DB 5; Length 78; 52.6%; Pred. No. 0.8; tive 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                             1015 AA; 112051 MW; FC6A756029C868F1 CRC64;
                                                                                                expression analysis in plasmodia treated with cAMP.";
Gene 209:39-44(1998)
BMBL, AF023910; AAC14193.1; -.
INTERPL, PLI379; 1A35.
InterPro; IPR001631; Topismerse_I.
Pfam; PF01028; Topoisomerrase_I; I.
Pfam; PF02919; Topoisomer I. N; I.
PRINTS; PR00416; EUTPESMRASĒI.
SMART; SM00435; TOPEUC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 AA; 8067 MW; 8417971A6FEF050B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 KKEVKKEDTAKKDVKKEVKKETPKKTPAKRKAAESSSEESDF 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) BCDNA:LD1177 protein. BCDNA:LD21177 OR CG8431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KKYAKKEKAAKKAYKKE------AKAKAAEAAKEAAY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 AKKRAAPKKKPAAKKAVNKSAKKHAAKKAPKKAVKKA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYA---KKEKAAKKAYKKEAKAKAAEAAKEAAYEA
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                        42.2%;
42.9%;
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 42.99
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                              somerase.
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                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           095UN5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=A3[2] / M145;
STRAIN=A3[2] / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";

Nature 417:141-147(2022)

EMBL; AL078618; CAB44532.1; -.

ELL FPFO, IPRO00064; NLPC P60.

Pfam; PPFO0877; NLPC P60; I.

SEQUENCE 277 AA; 27694 MW; C53669505187B256 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.2%; Score 70; DB 16; Length 277;
54.3%; Pred. No. 2.5;
tive 1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                         Saunders D.C., Harris D.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1015 AA
                                                                                                  Putative NLP/P60 family secreted protein. SCO4561 OR SCD16A.22. Streptomyces coelicolor.
                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                      01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TrEMBLrel. 02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA topoisomerase I.
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                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                            NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                      STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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ä

Gaps

3;

SEQUENCE FROM N.A

Physarum polycephalum (Slime mold). Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;

Physarum. NCBI\_raxID=5791; [1]

094705

RESULT 11
024705
DD 0Q4700
AC 0Q4700
DT 01-FE
DT 01-DE
DE DNA t
GN TOP1.
CS PHYSA
OC BUKAT
OC PHYSA
OC PHYSA
OX (1)

Matches

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Last sequence update)
Last annotation update)

Created)

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PRELIMINARY;
                        095UN6;
                9ND560
RESULT 14
       Q95UN6
ID Q9
AC Q9
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83 AA.

PRT;

Gaps

5,

6; Indels

4; Mismatches

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEA 31

셤 ઠે

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Trypanosoma cruzi.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                           Porto R.M., Amino R., Elias M.C.Q., Faria M.B., Schenkman S.; "Histone HI is phosphorylated in non-replicating and infective forms Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY046273; AALO2282.1; -... 83 83 83 83 85QUENCE 83 AA, 8592 MW; 7PAD924B1A6BD92E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Histone Hl protein.
Leishmania braziliensis.
Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYA---KKEKAAKKAYKKEAKAKAAEAAKEAAYEA:35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 AKKRAAPKKKPAAKKAVTKSAKKHAAKKAPKKAVKKA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
   01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.6
Matches 20; Conservative
                                                                                             Histone H1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                    STRAIN=Y;
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                                         RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortern J.R., Yandell M.D., Zhang Q., Chen L.X., R.A. Aradon R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortern J.R., Yandell M.D., Zhang Q., Chen L.X., Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champo M., Fefeiffer B.D., R.A. Anni J.F., Agbayani A., An H.-J., Andrews-Feankoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayakaracju L., Beasley E.M., Ballew R.M., Basu A., Bardell J., Bayakaracju L., Beasley E.M., Ballew R.M., Botchan M.R., Bouch J., Butler H., Cadieu E., Center A., Chandra I., R. A., Cayley S., Dahlke C., Davenport L.B., Davies P., A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A. Decker M., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P., Burtis N.L., Evangelista C.C., Ferraz C., Ferraz C., Ferraz C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Gong F., Gorrell J.H., Gu Z., Genner M.-H., Thegwam C., Julian A.E., Karpen G.H., Wei M.-H., Ibegwam C., Julian M.B., Houstin D., Houston K.A., Helman T.J., Hermandez J.R., Harris M.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C., Juliako P., Lei Y., Levitsky A.A., Li J., Li Z., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z., Liang Y., Lin X., Matterla B., McIntoch T.C., McLeodo M.P., McDherson D., Nelson D.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Welberson D., Nelson D.K., Nelson M., Pittman G.S., Pan S., Pollard J., Puri V., Reenington K.A., Nixon K., Nusskern D., Puri V., Reenington K., Sauderson M., Stunskern D., Sunith T., Saiden-Kamos I. Singerom M., Stunskern D., Sunith T., Saiden-Kamos I. Sunisson M., Stunskern K., Sainer K., Wassarman D.A., Walley K.C., Wu D., Yang G., Zho Q., Zho Q.A., Walley R., Zaveri J.S., Zhong G., Zho Q., Zho Q., Zho Q., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C., Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E., Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M., Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M. Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.6%; Score 69; DB 5; Length 741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AE003808; AAFS8057.1; -. EMBL; AF132160; AAD34748.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    741 AA; 84257 MW; 73D758634149385F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBGN0027536; BCDNA:LD21177.
InterPro:, IPR002308; Cys tRNA synt_la.
Pfam; PF01406; tRNA-synt_le; 1.
PRINTS; PR00983; TRNASYN<sup>T</sup>HCYS.
                                MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMB; TIGR00435; cysS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.3%;
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
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ij

Gaps

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Score 68.5; DB 5; Length 83; Pred. No. 1.1; 3; Mismatches 12; Indels

41.3%;

112 AA.

PRT;

PRELIMINARY;

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'n
                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                          41.3%; Score 68.5; DB 5; Length 112; 55.3%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                               Indels
STRAIN=MOHM/PE/95/LQ8;
Alonso V., Martinez E., Carmelo E., Pinero J., Gonzalez Ortega A., Valladares B.;
"H1 from Leishmania braziliensis.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF131892; AAD26570.1; -.
InterPro; IPR001386; Histone_H1/H5.
PRINTS; PR00624; H1STONEH5.
SEQUENCE 112 AA; 11370 MW; 1657D5D106C2DB80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             74 AKKSAPKKAVKKAVKAAKKAVKKAAK-KATKRTAKKAA 110
                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKE-----KAAKKAYKKEAKAKAAEAAKEAA 32
                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: March 10, 2003, 12:25:52 Job time : 20.5338 secs
                                                                                                                                                                                                                                                                 Local Similarity
nes '21; Conservative
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                               Matches
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Carmelo E., Pinero J., Gonzalez A., Zurita A.,

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-816-989A-1 Perfect score:

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

908470 segs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Databa

A_Geneseq_101002:*	1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*	2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*	IDS2/gcgdata/	4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*	5: /SIDS2/gcgdata/geneseg/genesegp-embl/AA1984.DAT:*	rps2/	7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*	8: /SIDS2/gcgdata/geneseg/genesegp-embl/AA1987.DAT:*	9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*	10: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*	<pre>11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*</pre>	12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*	13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*	14: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*	/gcgdata/		IDS2/	IDS2/	20: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*	22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*	23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
: 981																					

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Coolemen molecula	Copolymer molecula	C albicans apoptos	Recombinant copoly	Peptide modulating					
SUMMARIES			£	AAY82571	AAY82572	AAY82576	AAY82574	AAY82577	AAY82573	AAY82575	AAG70868	AAR06445	AAB08170
			DB	21	21	21	21	21	21	21	22	11	21
			Length	35	45	86	99	109	56	77	427	154	40
	ф	Query	Score Match Length DB I	100.0	65.1	65.1	63.6	63.3	63.0	63.0	52.1	45.8	44.3
			Score	166	108	108	105.5	105	104.5	104.5	86.5	16	73.5
		Result	No.	1	8	ო	4	S	9	7	80	σ,	10

Recombinant copoly	Human protein segu	C glutamicum prote	Drosophila melanog	Polycationic polyp	Protamine-like pep	Peptide modulating	Polycationic polyp	Protamine-like pep	Drosophila melanog	Human endometrial	Arabidopsis thalia	0		Arabidopsis thalia	ø	Arabidopsis thalia	M. tuberculosis hi	Н	Drosophila melanog		Drosophila melanog	3	Streptococcus pneu	Mycobacterium bovi	Enterococcus faeca	Enterococcus faeca	Breast cancer asso	Drosophila melanog	Drosophila melanog	ņ	Polycationic polyp	Protamine-like pep	e-like	T. cruzi L19E homo
AAR06446	AAM25508	AAG91997	ABB62028	AAR90180	AAW06686	AAB08168	AAR90181	AAW06688	ABB61894	AAU84310	AAG37166	AAG38490	AAG37165	AAG38489	AAG37164	AAG38488	AAY34055	AAY57353	ABB63417	AAY14928	ABB59960	AAG91846	AAW14537	AAB20575	AAU34982	AAU33397	AAY07029	ABB62173	ABB71574	AAR90176	AAR90178	AAW06687	AAW06697	AAW06913
7		~	N	٢	٦	7							21						22												16			17
106	146	165	741	32	32	32	33	33	515	582	242	242	245	245	300	300	214	214	481	223	322	498	203	205	169	782	621	607	2451	29	29	53	53	262
•	41.9	41.9	•	40.7	40.7	40.7	40.7	40.7	40.4	•	•	•		•	•	•	•	•	39.8	•	•	•	٠	•	38.9		٠	œ.	٠		37.7			37.7
71	69.5	ď.	69	۲.	۲.	۲.	•	~	67	66.5	99	99	99	99	99	99		65.5	65.5	65	65	S	64.5				63.5	63	63		62.5			62.5
11	12	13	. 14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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glatifamer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiboriatic; dermatory; antidiabetic; thyromimetic; haemostatic; antiboriatic; dermatory; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                    Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.
                                                                                                                                                                                           Copolymer; molecular weight marker; TV-marker; immune disease;
                                     AAY82571 standard; peptide; 35 AA.
                                                                                                               28-JUL-2000 (first entry)
                                                                            AAY82571;
RESULT 1
                 AAY8257
```

Unidentified

06-APR-2000.

WO200018794-A1

99WO-US22402. 24-SEP-1999; 98US-0101693. 25-SEP-1998;

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acctate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinits, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthemia gravis, psendiated diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated to the contact sensitivity diseases which can be treated to the contact sensitivity contact sensitivity can be can be treated to the contact sensitivity can be contacted to th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                        Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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100.0%; Pred. No. 9.3e-13;
live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 14; 72pp; English.
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                                                                                                                                   WPI; 2000-317499/27.
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Lis D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
Gad A,
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The colypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune complete which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, candemia, autoimmune opportitis, osteoarthritis, autoimmune haemolytic andemia, autoimmune opportitis, autoimmune thrombocytopaenia cuverrainis, contact sensitivity disease, diabetes mellitus, Graves purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves (Gisease, Guillain-Barres s syndrome, Hashimoto's disease, and myschemic gravis, psoriated diseases which can be treated include type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to all and an analogous to an analogous to an analogous to all and an analogous to all and an analogous to all and an analogous to an analogous to all and an analogous and an anal

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

WPI; 2000-317499/27.

Lis D;

Gad A,

25-SEP-1998; 98US-0101693

Claim 10; Page 14; 72pp; English.

Query Match
Best Local Similarity 100.
Matches 35; Conservative ઠે 셤

molecular weight markers.

45 AA;

Sequence

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glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyvoid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antiporniatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rhemmatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura, collitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
                                                                                                                                                       Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.
                                                                                                                                                                                              Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                      Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
pemphigus vulgaris; systemic lupus erythematosus.
                                    AAY82572 standard; peptide; 45 AA
                                                                                                              28-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                           AAY82572;
RESULT 2
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syndrome; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                 glatitamer acctate; autoimmume disease; antiatrhritts; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiporiatic; dermatory; antidiabetic; thyromimetic; haemostatic; antiporiatic; dermatoriogical; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                             Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.
                                           10;
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Score 108; DB 21; Length 45;
Pred. No. 6.7e-06;
1; Mismatches 5; Indels 1
                                                                                  1 AKKYAKKEKA--AKKAYK-----KEAKAKAAEAAKEAAYEA 35
                                                                                                                            1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAKEAAYEA 45
                                                                                                                                                                                                                                   AAY82576 standard; peptide; 86 AA
    65.18;
                                                                                                                                                                                                                                                                                                                   28-JUL-2000 (first entry)
    Query Match
Best Local Similarity 64.4
Matches 29; Conservative
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Unidentified

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AAY82577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for and an amino acid composition are used as molecular weight markers for Jatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or tribody-mediated diseases. Such diseases include arthritic conditions, demyellinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic ansemia, autoimmune opportitis, autoimmune thyroiditis, autoimmune autoimmune autoimmune autoimmune thyroiditis, autoimmune aut
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                                                                                                                                                                                                                                                                                                                                         Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.1%; Score 108; DB 21; Length 86; 57.4%; Pred. No. 1.3e-05; ive 2; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 14; 72pp; English.
                                                                                                                                                                            (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
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Best Local Similarity 57.4
Marches 27; Conservative
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WO200018794-A1
                                                                                                                                                                                                                                                      Lis D;
                                                                                                                                    25-SEP-1998;
                                                                                         24-SEP-1999;
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or artibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chomic immune thyroiditis, autoimmune thyroiditis, autoimmune purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            include host-versus-graft disease, graft-versus-host disease, and delayde-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
pemphigus vulgaris; systemic lupus erythematosus.
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43.9%; Pred. No. 1.9e-05;
iive 2; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 14; 72pp; English.
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Best Local Similarity
Matches 29; Conserv
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                                                                                                                 Unidentified,
                                                                                                                                                                                                                                                                                                                                                              24-SEP-1999;
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glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crown; a disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; (dillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                            Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
          Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                        pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 14; 72pp; English.
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                                                                                                                                                                                                                                                                                                               Lis D;
                                                                                                                                                                                                                                                25-SEP-1998;
                                                                                                                                               Unidentified
                                                                                                                                                                                                                       24-SEP-1999;
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                                                                                                                                                                                                                                                                                                               Gad A,
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune classes which may be treated include either cell-mediated or rational diseases such inflammatory conditions, e.g. multiple antibody-mediated diseases. Such disease include arthritic conditions, canaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune baemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, crohu's disease, chronic immune thrombocytopaenia uveoretinitis, contact sensitivity disease, diabetes mellitus, Graves purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, myasthenia gravis, psyndrome, Hashimoto's disease, and indopathic myxoedema, myasthenia gravis, psyndrome, Hashimoto's disease, and colled host-versus-graff disease, graff-versus-sqraff disease, called host-versus-graff disease, diabetes which can be treated include host-versus-graff disease, properties which are analogous to called the molecular weights and physical properties which are analogous to called the manufacture and properties which are analogous to called the manufacture and properties which are analogous to a sense the mideated manufacture and properties we as a sense of the invention have 109 AA; Sequence

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63.3%; Score 105; DB 21; Length 109; 62.2%; Pred. No. 3.6e-05; cive 2; Mismatches 5; Indels 10
                                  Conservative
                 Similarity
                                  28;
 Query Match
Best Local 8
                                Matches
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1 AKKYAKKEKAAKKAY----KKEA----KAKAAEAAKEAAYEA 35

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AAY82573 standard; peptide; 56 AA. AAY82573 ID AAY8 XX RESULT 6

AAY82573;

(first entry) 28-JUL-2000 Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.

glatifamer acctate; autoimmune disease; antiathitic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antibaoriatic; dermatory; antidanemic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; (frohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guilain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer; molecular weight marker; TV-marker; immune disease;

Unidentified

WO200018794-A1. 

06-APR-2000.

99WO-US22402. 24-SEP-1999;

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC. 98US-0101693. 25-SEP-1998;

Lis D; Gad A, WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

Claim 10; Page 14; 72pp; English

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight cf acopolymer (CP), which has an identified molecular weight cf acopolymer (CP), which has an identified molecular weight cand an amino acid composition corresponding to the copolymer. The colypeptides of the invention are used as molecular weight markers for glatinamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune corresponding to the acopolymer and include either cell-mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple aclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thrombocytopaenia cuvecretinitis, contact sensitivity disease, diabetes mellitus, Graves Guesase, Guillain-Barre's syndrome, Hashimoto's disease, diabetes mellitus, craves comycodema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delined molecular weights and physical properties which are analogous to colline the manner acetate molecules, which makes them ideal for use as

56 AA; Sequence

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Gaps

10;

21; Gaps 63.0%; Score 104.5; DB 21; Length 56; 51.8%; Pred. No. 2.1e-05; ive 4; Mismatches 2; Indels 21 29; Conservative Local Similarity Query Match Best Loca Matches

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1 AKKYAKKEKA----AKKAYKK-------EAKAKAAEAAKEAAYEA 35

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidianemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Pashinoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                     Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.
                                                                                          AAY82575 standard; peptide; 77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US22402.
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                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lis D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-SEP-1999;
                                                                                                                                                                                                                                                                                     28-JUL-2000
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                                                                                                                                                                                     AAY82575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gad A,
                                   AAY8257
RESULT
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The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia and neurodegeneration. The present sequence is one of the C. albicans proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 427;
                                                                                                                                                                                                          Yeast, fungus, apoptosis, infection, proliferative disease, vaccine, autoimmune disease, ischaemia, neurodegeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant copolymer 1-77, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                           Luyten WHML, Malcorps IKL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8;
35
              40 AKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 86.5; DB
Pred. No. 0.02;
1 AKKYAKKEKAAKKAY---KKEAKAKAAEAAKEAAYEA
                                                                                                                                                                                C albicans apoptosis associated protein #48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 KEKAKKEKAAKKWEKESGSRKAAEEAARKKAAEEA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKYAKKEKAAKKAYKKEAKAKAA-EAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.02
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 24; Fig 2; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR06445 standard; protein; 154
                                                                                               AAG70868 standard; Protein; 427
                                                                                                                                                                                                                                                                                                                                                                                                                          De Backer MD,
Reekmans RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 52.1%;
Local Similarity 65.7%;
hes 23; Conservative 3
                                                                                                                                                                                                                                                                                                                                         03-JUL-2000; 2000WO-BE00077.
                                                                                                                                                                                                                                                                                                                                                                   99EP-0870141.
                                                                                                                                                    27-JUL-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-367042/38.
N-PSDB; AAH29904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427 AA;
                                                                                                                                                                                                                                                     Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       certain diseases
                                                                                                                                                                                                                                                                                 WO200102550-A2
                                                                                                                                                                                                                                                                                                                                                                                                                          Contreras RH,
Nelissen BJM,
                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1999;
                                                                                                                                                                                                                                                                                                            11-JAN-2001
                                                                                                                           AAG70868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
Matches
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                                                                   RESULT
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1;

Gaps 3;

63.0%; Score 104.5; DB 21; Length 77; 65.8%; Pred. No. 2.9e-05; ive 4; Mismatches 6; Indels 3

25; Conservative

Matches

Query Match Best Local Similarity

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The present sequence represents a synthetic peptide which has a high affinity for glycoaminoglycans and proteoglycans. The peptide is useful in methods for modulating heparin or other glycoaminoglycans with anticoagulant activity, promoting cell attachment or adhesion to natural or synthetic surfaces (especially vein grafts), modulating curfunds differentiation, targeting drugs to epithelial cell surfaces (or to other cells expressing proteoglycans), modulating enzymes that act on glycoaminoglycan grafting proteoglycans, modulating enzymes that act on glycoaminoglycan atti-coagulant functions mediated through glycoaminoglycans, and anti-coagulant functions mediated through glycoaminoglycans, and tissue uptake of heparin or other glycoaminoglycans, and tissue uptake of heparin or other glycoaminoglycans in a mammal to increase heparin half-life in circulation.
                                                                                                                                                                                                                                                                                                                            Novel synthetic peptides with high affinity for glycoaminoglycans and proteoglycans, useful for modulating heparin, promoting cell attachment, modulating tumour metastasis and modulating wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             copolymer 1; COP-1-19; myelin basic protein; MBP; 1 activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.3%; Score 73.5; DB 21; Length 40; 61.1%; Pred. No. 0.061; ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant copolymer 1-19, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KKAAKAARKKAAKKAARKKAARKAAKAARKAA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKYAK--KEKAAKKAYKKEAKA---KAAEAAKEAA 32
                                                                                                                                                                                                                                               Schick BP;
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 30; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR06446 standard; protein; 106 AA
                                                                                                                                                                                                                                               Verrecchio A,
                                                                                                                                                                                                    (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                           99US-0118276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90US-0473845.
89US-0312541.
                                                                                                             02-FEB-2000; 2000WO-US02853.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 61.1 tes 22; Conservative
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                                                                                                                                                                                                                                                                                          WPI; 2000-543446/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunological active multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 AA;
                                                                                                                                                                                                                                               San Antonio JD,
                         WO200045831-A1
                                                                                                                                                           02-FEB-1999;
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                                                                    10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1.77 were subcloned from PREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US461009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences. the COP-1 polypeptide may be cleaved from the fusion protein. the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1.77 contains oligonuclectide duplexes incoding the following segments: YKK, EAB, KAK, AAK, and AAA. The N-terminal alanine residue is left behind following CABL and an and an anticonsimants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoaminoglycan; proteoglycan; heparin modulation; anticoagulant; cell attachment; cell adhesion; vein graft; tumour cell metastasis; cartilage differentiation; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity
Recombinant copolymer 1, COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide modulating activity of heparin, and other glycans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.8%; Score 76; DB 11
54.1%; Pred. No. 0.12;
iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KKYAKKEKAAKKA----YKKEAKAKAAEAAKEAAYE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 KKKAKEAEKAKKAKYKKYKKKEAEAAKAAKAAAAAYK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 11; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB08170 standard; peptide; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match. 45.8%;
Best Local Similarity 54.1%;
Matches 20; Conservative
                                                                                                                                                                                                                        90EP-0301700.
                                                                                                                                                                                                                                                                 90US-0473845.
                                                                                                                                                                                                                                                                                          89US-0312541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                 (REPL-) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1990-255848/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             certain amino acids.
See also AAQ05665.
                                         multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ05664.
                                                                                                                                                                                                                        16-FEB-1990;
                                                                                                                                                                                                                                                                                          17-FEB-1989;
                                                                                                                                                                                                                                                                   07-FEB-1990;
                                                                                                                                                                             22-AUG-1990
                                                                                                                                 EP383620-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Syntheric.
                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB08170;
                                                                                                                                                                                                                                                                                                                                                                            Cook KS;
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RESULT 10 AAB08170 ID AAB0

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7

Gaps

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Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -

Tang YT, Liu C, Drmanac RT

(HYSE-) HYSEQ INC.

2001-457603/49.

N-PSDB; AAH99449

23-DEC-1999; 99US-0471275. 21-JAN-2000; 2000US-0488725. 25-APR-2000; 2000US-0552317.

22-DEC-2000; 2000WO-US35017.

26-JUL-2001.

Claim 20; Page 210; 1217pp; English.

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Human, cancer; ulcer, HIV infection; human immunodeficiency virus;

antibliflammatory; antitheumatic; antiarthrific; immunosuppressive;

M antibacterial; endocrine; cardiant; central nervous system; virucide;

antibacterial; endocrine; cardiant; central nervous system; virucide;

antiagregant; andocrine; cardiant; cardiant; antianaemic; anaman;

antiagregant; namostatic; vulnerary; antiulcer; osteopathic; eczema;

dermatological; antidepressant; noctropic; antidaptic; cytostatic;

meuroprotective; antidepressant; noctropic; antidarkinsonian; infection;

immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;

antianaphylactic; rheumatolid arthritis; septic shock; pancreatitis;

cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;

genetic disease; haematopoietic disorder; platelet disorder; asthma;

Alregic rhinitis; diabetes; multiple sclerosis; depression;

Alrefiner's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                        coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-19 contains oligonucleocited duplexes incoding the following segments: YKK, AAE, KAK, EKA, KKA, YEA, AKA KEA, and AAA. The herminal alanine residue is left behind following CNBr cleavage of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control ademyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                - for
                                                                                                                                                                                                                                                      To improve the expression of rCOP-1 polypeptides in E. coli,
                                                                                                                          Producing genes encoding random polymers of aminoacid(s) - f
producing recombinant polypeptide(s) with biological and/or
immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.8%; Score 71; DB 11; Length 106;
48.9%; Pred. No. 0.32;
ive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------KAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KAAEKAKAAKKAYEAEKAKAEKAEKAEKAEKAAAEKKAKE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein sequence SEQ ID NO:1023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM25508 standard, Protein; 146 AA
                                                                                                                                                                                                                Disclosure; Fig 12; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KYAKKEKAAKKAYKKE-AKA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 48.9
nes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological disorder.
                                                              WPI; 1990-255848/34.
N-PSDB; AAQ06446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               See also AAQ05664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200153455-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                   Cook KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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AAM259166 to AAH99904 encode the human proteins given in AAM25225 to
AAM25933. The proteins can have activities based on the tissues and
cells they are expressed in, such as: antinifammatory; antipheumatic,
antiarthritc; immunosuppressive; antibacterial; endocrine; cardiant;
cardiovascular; antianaemic; antiageregant; haemostatic; vulnarary;
cardiovascular; antianaemic; antiageregant; haemostatic; vulnarary;
cardiovascular; antianaemic; antiageregant; nactiallergic; antiasthmatic;
antidleer; osteopathic; dermatological; antiallergic; antidathmatic;
antidlear; osteopathic; dermatological; antiallergic; antidated antidiapetic; cytostatic; neuroprotective; antidepressant; nootropic;
antidiapetic; cytostatic; neuroprotectides are useful for screening for groduction, The proteins and polynucleotides are useful for screening for agondates associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis; severe combined infections, autoimmunity, cancer, multiple sclerosis, depression, contended antimunodeficiency, eczena, allergic
antimularia, asthma, diabetes, cancer, multiple sclerosis, depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 41.9%; Score 69.5; DB 22; Length 146; Best Local Similarity 52.6%; Pred. No. 0.65; Matches 20; Conservative 4; Mismatches 9; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C glutamicum protein fragment SEQ ID NO: 5751.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYAKKEKAAKKA----YKKEAKAKAAEAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG91997 standard; Protein; 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2000; 2000EP-0127688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurological disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1108790-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG91997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG91997
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher everaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                               Disclosure, SEQ ID NO 12876; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                   41.6%; Score 69; DB 22; Length 741; 61.3%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                            649 AKLAABAEKARAAEKERKKQAAAEA--AAAKEA 677
                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEA 31
                                                                                                                                                                                                                                                                                                                                                  19, Conservative
WPI; 2001-656860/75.
N-PSDB; ABL06131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-193899/25.
                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                        (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                            741 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9513083-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .0-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andrews PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR90180;
                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                         The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the Buropean Patent Office.
                                                                                                                                                                              Novel polynuclectides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 5
                                                                                                                                                                                                                                                  Claim 17; SEQ ID NO: 5751; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 165;
                                                                                             Mizoguchi H, Ando S, Hayashi M, Ochiai K,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 12876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 KKKAREDKEAKEAAEKAAAEKAAAAESEEAPAEEAAAE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KKYAKKEKAAKKAYKKEAKAKAA-----EAAAKEAAYE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 69.5; DB Pred. No. 0.74; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB62028 standard; Protein; 741 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PWD,
                                                                   (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.9%;
                          07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
              99JP-0377484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0°
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC, Adams M,
                                                                                                                                       2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 AA;
                                                                                                                                                    N-PSDB; AAH67216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical
                                                                                             Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB62028;
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Gaps

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Indels

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4; Mismatches

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New poly:cationic polypeptide n-protamine analogues - having reduced cationic charge and lower toxicity, used for reversing low mol.wt.
                                                                                                                                                                                                             n-protamine, anticoagulation reversal; low molecular weight heparin; polycationic; positively charged amino acid; lysine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "C-terminal is in amide form"
                                                                                                                                                                                                                                                                                                                                                                                                               'note= "N-terminal is acetylated"
                                                                                                                                                                 Polycationic polypeptide n-protamine analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŢW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wakefield
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 13; 34pp; English
  ¥.
AAR90180 standard; peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0303025.
93US-0152488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94WO-US12981
                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stanley JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heparin anticoagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UNMI ) UNIV MICHIGAN.
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us-09-816-989a-1.open.rag

Novel peptides are claimed which contain 20-40 amino acids and which have a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as determined by the number of positively charged amino acids in the sequence. Preferably the positive charges are grouped amino acids amono acids having blocks of 2-4 positively charged amino acids amino acids having blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of the protains (total cationic charge = +21) in which selected arginine residues have been replaced with uncharged amino acids and other arginine residues have been replaced by other positively charged amino acids and other arginine residues have been replaced by other positively charged amino acid residues, the fearbly lysine. The peptides reverse the effect of low mol. Wt. heparin (LMMH) anticoagulation and hence can be used medically to prevent bleeding are less toxic than n-protamine since the reduced positive charge gives an improved efficiency to toxicity ratio; and they may be more effective than n-protamine in their anti-LMMH action.

The present sequence (total cationic charge = +18) is a specific example of the new polypeptides. 32 AA; Sequence XCCCCCCCCCCCCCCCCCCCCCCCC

Gaps 1, Query Match
40.7%; Score 67.5; DB 16; Length 32;
Best Local Similarity 61.3%; Pred. No. 0.24;
Matches 19; Conservative 2; Mismatches 9; Indels 1

..

2 AKKAAKKAAKKAAKKAAKKAKKAAKKAKK 32

Search completed: March 10, 2003, 12:21:27 Job time : 19.2384 secs

1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30 δ 요

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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March 10, 2003, 12:26:10 ; Search time 10.4114 Seconds
(without alignments)
141.764 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-816-989A-1 Perfect score:

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35 Sequence:

188354 seqs, 42170167 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters:

188354

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:\*
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW PUB.pep:\*
3: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW PUB.pep:\*
4: /cgn2\_6/ptodata/1/pubpaa/USO6\_PUBCOMB.pep:\*
5: /cgn2\_6/ptodata/1/pubpaa/USO7\_NEW PUB.pep:\*
6: /cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*
7: /cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*
8: /cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
9: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
10: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
11: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
12: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
11: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
12: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
13: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 1, Appli		6	4	7	Sequence 3, Appli	,	⋖		Sequence 100, App	Sequence 201, App	$\boldsymbol{\circ}$	Sequence 10575, A	Sequence 4893, Ap	Sequence 7, Appli	Sequence 24, Appl	Sequence 27, Appl	Sequence 9, Appli	Semience S April 1
	ID	US-09-816-989A-1	US-09-816-989A-2	US-09-816-989A-6	US-09-816-989A-4	US-09-816-989A-7	US-09-816-989A-3	US-09-816-989A-5	US-09-820-843A-8	US-09-738-626-5751	US-09-919-497-100	US-10-051-643-201	US-09-738-626-5600	US-09-815-242-10575	US-09-815-242-4893	US-10-093-892-7	US-09-820-843A-24	US-09-820-843A-27	US-10-093-892-9	TIS-10-093-892-5
	DB	107	10	70	10	10	10	10	6	σ	10	σ	9	10	10	σ	σ	Φ	σ	σ
	Query Match Length DB	35	45	98	99	109	56	77	372	165	582	223	498	769	782	96	309	356	96	105
<b>J</b> P	Query Match	.100.0	65.1	65.1	63.6	63.3	63.0	63.0	44.6	41.9	40.1	39.2	39.5	38.9	38.9	37.3	37.0	35.8	35.5	35.5
	Score	166	108	108	105.5	105	104.5	104.5	74	69.5	66.5	65	65	64.5	64.5	62	61.5	59.5	59	59
	Result No.		7	m	4	S	9	7	æ	0	10	11	12	13	14	15	16	17	18	13

<u>m</u>		Sequence 12759, A Sequence 5289, Ap Sequence 12235, A Sequence 5198, Ap	Sequence 2, Appli Sequence 35241, A Sequence 225, App Sequence 95, Appl Sequence 45765, A	Sequence 229, App Sequence 4, Appli Sequence 4122, Ap Sequence 6, Appli	Sequence 6, Appli Sequence 36182, A Sequence 147, App Sequence 190, App Sequence 262, App
10 US-09-815-242-10314 9 US-09-999-724-90 9 US-09-999-724-46 9 US-09-999-724-48	9 US-09-82C-843A-23 10 US-09-92C-30O-1164 9 US-10-184-832-5 10 US-09-81S-242-13765	10 US-09-815-242-12759 10 US-09-815-242-5289 10 US-09-815-242-12235 10 US-09-815-242-5198	9 US-10-117-604-2 10 US-09-864-761-35241 10 US-09-764-846-225 9 US-09-820-843A-95 10 US-09-864-761-45765	9 US-10-002-344A-229 9 US-10-141-627-4 9 US-09-738-626-4122 9 US-10-141-627-6	1 US-08-325-278-6 10 US-09-864-761-36182 10 US-09-764-846-147 10 US-09-764-846-190 10 US-09-764-846-262
890 102 118 218	307 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	220 220 840	63 150 369 41	76 254 276 284	443 617 39 74 74
3 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	33.7 33.7	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	33333 33335 345 35 35 35 35 35 35 35 35 35 35 35 35 35	32.5 32.5 32.5	322.5 31.0 31.0 31.0 6.0
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## ALIGNMENTS

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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK)

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT FILING DATE: 1998-09-25

PRIOR APPLICATION NUMBER: 60/101,693

PRIOR APPLICATION NUMBER: 60/101,693

PRIOR APPLICATION NUMBER: 97/US99/22402

PRIOR APPLICATION NUMBER: 97/US99/22402

PRIOR PILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PALENT NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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ilarity 100.0%; Pred. No. 2.4e-13;
Conservative 0; Mismatches 0;
Sequence 1, Application US/09816989A, Patent No. US20020115103A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                              APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 35; Conserv
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Indels 1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35 1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35 Sequence 2, Application US/09816989A, Patent No. US20020115103A1, GENERAL INFORMATION:
APPLICANT: Gad, Alexander APPLICANT: Lis, Doris US-09-816-989A-2 g 8

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Sequence 7, Application US/09816989A
; Sequence 7, Application US/09816989A
; Patent No. US20020115103A1
; GENERAL INPORMATION:
    APPLICANT: Lis, Doris
    APPLICANT: Lis, Doris
    TITLE OF INVENTION: COPCLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT FILING DATE: 2004-03-23
; PRIOR FILING DATE: 1998-09-25
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SGOTWARE PATENCENTION NUMBER: PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09816989A

PREENT NO. US202015103A1

GENERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: List, Doris

ITILE OF INVENTION:

TITLE OF INVENTION:

AND FOR THERAPEUTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 109;
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Best Local Similarity 62.2%; Pred. No. 8.8e-06;
Matches 28; Conservative 2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.6%; Score 105.5; DB 10
Best Local Similarity 43.9%; Pred. No. 4.5e-06;
Matches 29; Conservative 2; Mismatches 4;
    CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 00/101,693
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 4
LENGTH: 66
TYPE: PRT
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-816-989A-7
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US-09-816-989A-3
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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23 PRIOR PILING DATE: 1998-09-25 PRIOR FILING DATE: 1998-09-25 PRIOR FILING DATE: 1998-09-24 NUMBER OF SEQ ID NOS: 7 SOFTWARE: PSEC ID NOS: 7 SEQ ID NOS: 7 SOFTWARE: PSEC ID NOS: 7 SEQ ID NOS: 7 SOFTWARE: PSEC ID NOS: 7 SEG ID NOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERABEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT FILING DATE: 12001-03-23
FRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 6
LENGTH: 86
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Patent No. US20020115103A1
GENERAL INPORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
FITLE OF INVENTION: AND FOR THERABEUTIC USE
FIGER REFERENCE: 2609/60807-A-PCT-US
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US-09-816-989A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 AKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAKAAKAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKEKA--AKKAYK-----KEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 АККУАККАКАЕКАККАУКААЕАККААКУЕКАААЕКАААКЕААУЕА 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 108; DB 10;
Pred. No. 1.6e-06;
1; Mismatches 5;
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Pred. No. 3.1e-06;
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; Sequence 6, Application US/09816989A
; Patent No. US20020115103A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.1%;
Best Local Similarity 64.4%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 27; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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Patent No. US20020106662A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REPRESENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
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41.9%; Score 69.5; DB 9; Length 165;
Best Local Similarity 50.0%; Pred. No. 0.17;
Matches 19; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                    DB 9; Length 372;
                                                                                                                                                           OTHER INFORMATION: outer membrane integrity protein (tola)
NAME/KBY: misc feature
COTHER INFORMATION: gi | 1573353
US-09-820-843A-8
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KKYAKKEKAAKKAYKKEAKAKAA----EAAAKEAAYE 34
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.1%; Pred. No. 0.12
Matches 18; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 5751
LENGTH: 165
                                                                                                                                                                                                                                                                                                                                                                                                   5 AKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5751, Application US/09738626
Publication No. US20020197605A1
GENERAL INPORMATION:
APPLICANT: MAKAGAWA, SATOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5751
           SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
                                                                         TYPE: PRT
ORGANISM: H. influenzae
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-919-497-100
                                 SEQ ID NO 8
LENGTH: 372
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; Patent No. US20020115103A1
; GENERAL INPORMATION:
APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2609/60807-A-PCT-US
; CURRENT FILING DATE: 1998-09-25
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Version 3.1
; SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09820843A
Publication No. US20030039963A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEITITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
CURRENT APPLICATION WHERE: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                              5
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                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          Score 104.5; DB 10;
Pred. No. 5e-06;
4; Mismatches 2; :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 104.5; DB Pred. No. 7e-06;
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
FRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.0%;
                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 51.8%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 65.8
Matches 25; Conservative
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US-09-816-989A-5
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US-09-820-843A-8
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                                                                                                                                                                                                                                                                                                       FEATURE:
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Sequence 10575, Application US/09815242

Setent No. US20020061565A1

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Chisen, Kari L.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Wall, Daniel
APPLICANT: Wamanock, Bobert T.
APPLICANT: Yamanock, John D.
APPLICANT: Zoud-02-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-24
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-13-21
                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.2%; Score 65; DB 9; Length 498; Best Local Similarity 53.3%; Pred. No. 1.8; Matches 16; Conservative 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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38.9%; Score 64.5; DB 10;
Best Local Similarity 48.6%; Pred. No. 3.3;
Matches 17; Conservative 6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAK-KEKAAKKAYKKEAKAKAAEAAAKEAAYE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 AKKTARKAPAKKTVAKKATTAKAAPATAKD 113
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PELING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 5600
LENGTH: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKE 30
                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-815-242-10575
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US-09-815-242-4893
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Sequence 201, Application US/10051643

Sequence 201, Application US/10051643

Sequence 201, Application US/2020197265A1

Sequence 201, Application No. US20020197265A1

Septicant: Watson, James D.

APPLICANT: Watson, James D.

TITLE OF INVENTION: Paul L. J.

TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: System using Mycobacterium Vaccae

FILE REFERENCE: 11000-100862

CURRENT FILING DATE: 1000-100862

CURRENT FILING DATE: 1000-1016

PRIOR PAPLICATION NUMBER: US/91/56,181

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 208

SEQ ID NO 201

LENGTH: 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.2%; Score 65; DB 9; Length 223; 54.3%; Pred. No. 0.78;
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                                                                                                                                                                                                                                                                                              Query Match
40.1%; Score 66.5; DI
Best Local Similarity 48.6%; Pred. No. 1.4;
Matches 17; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                2 KKYAKKEKAAKKAYKK-EAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
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FILE REPRENCE: 249-125
CHRRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SEQ ID NO 100
LENGTH: 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRGANISM: Mycobacterium vaccae US-10-051-643-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Conservative
                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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US-09-738-626-5600
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US-10-093-892-7
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Pred. No. 3.4;
6; Mismatches 11; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLASER, Theresa Ann
TITLE OF INVENTION: IMMUNITY TO TRYPANOSOMATIDS SPECIES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: 91118bury Madison & Sutro
STREET: 1100 New York Avenue, N.W.
                                                                                               APPLICANT: Obligen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Tamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPRENCE: ELITRA 0.11A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAK-KEKAAKKAYKKEAKAKAAEAAAKEAAYE 34
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT AFFLIAGION NUMBER: 05/09/815,242
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FLING DATE: 2000-03-21
PRIOR FLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-22
PRIOR FILING DATE: 2001-22
PRIOR FILING DATE: 2001-27
PRIOR FILING DATE: 2001-22
PRIOR FILING DATE: 2001-22
PRIOR FILING DATE: 2001-22
PRIOR FILING DATE: 2001-22-6
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PSECSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 4893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/093,892
FLLING DATE: 11-Mar-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/10093892
Patent No. US/2002107/697A1
GENERAL INFORMATION:
APPLICANT: FASEL, Nicolas Joseph
Sequence 4893, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecalis US-09-815-242-4893
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                                                                              APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 38.9
Best Local Similarity 48.6
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-10-093-892-7
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37.3%; Score 62; DB 9; Length 96; ilarity 57.1%; Pred. No. 0.71; Conservative 1; Mismatches 10; Indels
APPLICATION NUMBER: US/08/668,255
FILING DATE: June 20, 1996
APPLICATION NUMBER: EP 96200665.6
FILING DATE: March 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Paul N. Kokulis
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 11422/224090
TELECPMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKK--EKAAKKAYKKEAK--AKAAEAAKEA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 AKKPAKKVAEKPAKKVVKKPAKKVVKKAVKAVKA 74
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: March 10, 2003, 12:53:42 Job time : 10.5543 secs
                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 96 amino acids
                                                                                                                                                                                                                                                                                 TELEX: 6714627
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Matches 20; Conserv
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Sequence 13, Appl Sequence 15, Appl Sequence 2, Appli Sequence 2, Appli Sequence 201, Appl Sequence 201, Appl Sequence 10, Appl Sequence 11, Appl Sequence 1
                                                                                                                                                                                                              March 10, 2003, 12:15:04; Search time 6.20253 Seconds (without alignments)
166.029 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
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US-08-373-025-15
US-08-373-025-15
US-08-33-025-16
US-08-33-025-16
US-09-035-855-201
US-09-095-855-201
US-08-152-488-10
US-08-152-488-10
US-08-152-488-11
US-08-152-488-11
US-08-152-488-11
US-08-152-488-11
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US-08-152-488-11
US-08-152-488-11
US-08-152-488-11
US-08-373-025-13
US-08-373-025-13
US-08-373-373-15
US-08-477-304-11
US-08-436-7038-3
US-08-436-7038-3
US-08-436-7038-15
US-08-436-7038-15
US-08-436-7038-15
US-08-436-7038-15
US-08-436-7038-15
US-08-677-309-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -08-834-306-51
-08-993-674A-51
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                     US-09-816-989A-1
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
No.
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1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
                                      2 AKKAAKKAKKAAKKAAKKAAKKAAKKAXK 32
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
TELEPAX: 908-276-5543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                    US-08-677-304-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-677-304-13
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                                                                                                                     Query Match

40.7%; Score 67.5; DB 1; Length 32;
Best Local Similarity 61.3%; Pred. No. 0.05;
Matches 19; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 40.7%; Score 67.5; DB 1; Length 32; Best Local Similarity 61.3%; Pred. No. 0.05; Matches 19; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wakefield, Thomas W.
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL CORRESPONDENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY.

CITY.

CITY.

SIREBI:

Detroit

STATE: Michigan

COUNTRY: United States of America

ZIP: 48226-4415

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: MS-DOS V.6.22

SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/303,025

FILING DATE: 08-SEPT-1994

CLASSIFICATION DATA:

APPLICATION NUMBER: PCT/US92/06829

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: 313-496-4545

INFORMATION FOR SEQ ID NO: 15:

TEMERATOR SEASON INFORMATION:

TELEFAX: 313-496-8454

INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Benita J, Rohm, Esg.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                      1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
                                                                                                                                                                                                                                                     2 AKKAAKKAKKAKKAAKKAKKAAKKA32
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-13
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US-08-303-025-15
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDENNESS: N/A
TOPOLOGY: N/A
MOLECTLE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
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Sequence 13, Application US/08677304
Patent No. 5721212
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: AAATEWS, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 61.3%; Pred. No. 0.05;
Matches 19; Conservative 2; Mismatches 9;
                                                                                                                                                                                                     NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Benita J, Rohm, Esq.
STRET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
COUNTY: United States of America
ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING LAIS:
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08669
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INPORMATION:
NAME: ROHM, Benita J.
REGISTRATION NUMBER: 28,664
FREGISTRATION NUMBER: 28,664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: No. 5721212 Relevant
TOPOLOGY: No. 5721212 Relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-08-436-703B-2
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APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: WRIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                STREET: 150 WEBE DEITETBON, SUITE 2500
CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy diskette 3.5" 1.44Mb
COMPUTER: DEAD COMPATIBLE
OPERATING SYSTEM: MS-DOS v.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIFICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AuG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
   NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
Bentia J, Rohm, Bsq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
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STATE: Michigan
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Benita J, Rohm, Esq. STREET: 6601 Woodward Avenue STREET: Suite 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-436-703B-4
; Sequence 4, Application US/08436703B
; Patent No. 5919761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 313-496-8454
INPORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: N/A
ORGANISM: N/A
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN AND TITLE OF INVENTION: ANTICOAGULATION REVERSAL
                                                                                               APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Andrews, Philip C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: WIGHT HEPARIN
TITLE OF INVENTION: WIGHT HEPARIN
TITLE OF INVENTION: WITCOAGULATION REVERSAL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, ESG.
STREET: Suite 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7WK-060548-00233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
ORPHARE: MOTORE
SOFTWARE: WOOTGPETECT 6;
SOFTWARE: WOOTGPETECT 6;
SOFTWARE: ASCII (DOS) TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: N/A
ATTONEN APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTONENY/ASTATION NUMBER: TWK-060548-007
REGISTRATION NUMBER: TWK-060548-007
TELECOMMUNICATION INFORMATION:
TELECOMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Michigan
COUNTRY: United States of America
ZIP: 48226
Sequence 2, Application US/08436703B
Patent No. 5919761
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 32 amino acids
TYPE: amino acids
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECILE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: N/A PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detroit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TITLE: N/A
US-08-436-703B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-08-303-025-16
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GENERAL INFORMATION:
GENERAL INFORMATION:
FAULICANT: Visser, Elizabeth
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Stinner, Margot
APPLICANT: Stinner, Margot
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Billott Avenue, Suite 4185
CCITY: Seattle
STATE: WA
CCOUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.5%; Score 65.5; DB 3; Length 214; Best Local Similarity 52.4%; Pred. No. 0.63; Matches 22; Conservative 3; Mismatches 10; IndelB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKK-----EKAAKKAYKKEAKAKAA-EAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastesEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/US/US/BSS
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-UN-1997
APPLICATION NUMBER: 08/897,362
FILING DATE: 23-DEC-1997
ATONNEY/AGENT INFORMATION:
NAME: Sleath Janet
REGISTRATION NUMBER: 37,007
REFERRICE/DOCKET NUMBER: 11000.1002c3
TELEPHONE: 266-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 201, Application US/09095855 Patent No. 6160093
                                            NAME: Cambell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFRENCE/DOCKET NUMBER: P-PM
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 and and acids
TYPE: and acids
TYPE: and acids
TOPOLOGY: linear
FILING DATE: 11-APR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEC ID NO:
                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-09-041-889-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-095-855-201
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Sequence 27, Application US/09041889

Patent No. 6033864

GENERAL INFORMATION:
APPLICANT: Chavy, Offer
APPLICANT: Chavy, Offer
TITLE OF INVENTION: Microbial UC panca antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
CITY: San Diego
STATE: California
COUWTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/837,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 40.7%; Score 67.5; DB 2; Length 33; Best Local Similarity 61.3%; Pred. No. 0.051; Matches 19; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7WK-060548-00233
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: TBM FC compatible
COMPUTER: TBM FC compatible
CORENATION SYSTEM: Ms-DOS
SOFTWARE: McTOREFECT 6;
SOFTWARE: ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERENCE/DOCKET NUMBER: 786,05548-0023
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 AKKAAKKAKKAAKKAKKAAKKAKK 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL TYPE: OUNCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: N/A PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TITLE: N/A
US-08-436-703B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-041-889-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08152488
Fatent No. 5534619
GENERAL INFORMATION:
APPLICANT: Wakefield Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
SIATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: MS-DOS
OSFWWARE: Wordberfect 6; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FLING DATE: 12-NOV-1993
CLASSIFICATION: 514
       WordPerfect 6; ASCII (DOS) Text
                                                   PPLICALLON
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROHM. Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-5344
INFORMATION: FOR SEQ ID NO: 10:
SEQUENCE CHARACTER/STICS:
LENGTH: 29 amino acids
"""" amino acid
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APPLICATION NUMBER: PCT/US92/08069
FILLIO DATE: 14-AUG-1993
ATTORNEY AGENT INFORMATION:
                                       UMBER: US/08/152,488
12-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-10
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECTLE TYPE: peptide
ORGHINAL SOURCE: peptide
ORGHNISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 62.1f
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: N/A
TITLE: N/A
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-08-152-488-11
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APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Diagnosis of Mycobacterial Infections FILE OF INVENTION: Diagnosis of Mycobacterial Infections FILE REPERBUCE: 11000.1002c4
CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT APPLICATION NUMBER: US/09/5,855
EARLIER PILING DATE: 1998-12-04
EARLIER PILING DATE: 1998-06-11
EARLIER PILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER FILING DATE: 1997-06-12
EARLIER FILING DATE: 1997-06-12
EARLIER FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
SOFTWARE PRESEE FEATSEQ for Windows Version 3.0
                                                                                             Query Match
39.2%; Score 65; DB 4; Length 223;
Best Local Similarity 54.3%; Pred. No. 0.75;
Matches 19; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65; DB 4; Length 223; Pred. No. 0.75;
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Fatent No. 5534619

GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Wakefield, Thomas W.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
                                                                                                                                                                                                                         1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
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COUNTRY: United States of America
ZIP: 07016-1811
                                                                                                                                                                                                                                                                                                                                                         ; Sequence 201, Application US/09205426; Patent No. 6406704; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQ ID NO 201
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-205-426-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 19; Conservative
i TOPOLOGY: linear
i MOLECULE TYPE: protein
US-09-095-855-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                            RESULT 9
US-09-205-426-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-08-152-488-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN AND TITLE OF INVENTION: MOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSES: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Detroit
STREET: Alow west Cetacook
COUNTRY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS V.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FLING DATE: 08-SEPT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERRINGE/DOCKET NUMBER: TWH-060548-00231
TELEFPAX: 313-496-7622
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acid
STRANDEDNESS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AKKAAKKAKKAAKKAAK-KAKKAAKK 29
                                                                                                                                           ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
ITILE: N/A
DOCUMENT NUMBER: PCT/US92/08069
FILLING DATE: 14-AUG-1993
           29 amino acide
                            TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: N/A .
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.7%; Score 62.5; DB 1; Length 29; 62.1%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08303025
Patent No. 564494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
TITLE OF INVENTION: NOWEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: NOWEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDED ADDRESS:
ADDRESSE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Detroit
STATE: Michigan
COUNTY: Detroit
ZIP: 4825-4415
COMPUTER: Wichigan
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: IRM PC compatible
OPERATING SYSTEM: MS-DOS v.6.22
SOFTWARE: Wordberfect 6.1; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CCASSIFTCATION: BTA
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-20-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm. Benita J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7WH-060548-00231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
TELEPHONE: 908-276-5543
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAAKKAYKKEAKAKAAEAAK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AKKAAKKAAKKAKKAAK-KAKKAAKK 29
                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-152-488-11
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-496-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Conservative
                                                                                                                                                                                                                                                                                                                               ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  N/A
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INFORMATION FOR
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US-08-303-025-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                 Sequence 10. Application US/08677304
; Sequence 10. Application US/08677304
; Patent No. 5721212
; GENERAL INFORMATION:
   APPLICANT: Wakefield, Thomas W.
   APPLICANT: Andrews, Phillip C.
   APPLICANT: Andrews, Phillip C.
   APPLICANT: Andrews, Phillip C.
   APPLICANT: Andrews, Phillip C.
   APPLICANT: ANDREWS.
   TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
   TITLE OF INVENTION: ANTICOAGULATION REVERSAL
   NUMBER OF SEQUENCES: 13
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Benita J, Rohm, Esq.
   STREET: 512 Springfield Avenue
   CITY: Cranford
   STAFE: New Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 6; ASCII (DOS) Text CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILING DATE:

FILING DATE:
CLASSIFICATION: 530

FRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488

FILING DATE: 12-NOV-1993

FILING DATE: 14-AUG-1993

ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28.664

REFERENCE/DOCKET NUMBER: 28.664

REFERENCE/DOCKET NUMBER: RM-7WG

TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-5344

TELEFAX: 908-276-5543

INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: No. 5721212 Relevant
TOPCLOGY: No. 5721212 Relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
      1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
                                                2 AKKAAKKAKKAKKAAK-KAKKAAKK 29
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DOCUMENT NUMBER: PCT/US92/08069
US-08-677-304-L0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 62.1?
Matches 18; Conservative
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PUBLICATION INFORMATION:
AUTHORS: N/A
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                                                                                                             37.7%; Score 62.5; DB 1; Length 29; 62.1%; Pred. No. 0.17;
                                                                                                                                                                                                                                                      Sequence 13, Application US/08303025
; Patent No. 5614494
; GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson CITY: Detroit
                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY.
CITY.
CITY.
CONTRY: United States of America
ZIP: Michigan
CONPUTER: Michigan
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: LEM PC Compatible
COMPUTER: WordPerfect 6.1; ASCII (DOS) Text
CONFRITA APPLICATION DATA:
PILING DATE: 08-SEPT-1994
CLASSIFICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIFICATION NUMBER: US/08/303,025
FILING DATE: 14-AUG-1992
RPPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERENCE/DOCKET NUMBER: 7WH-060548-00231
TELECHONE: 313-496-7622
                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                     1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
                                                                                                                                                                                                                                 2 AKKAAKKAKKAAKKAAK-KAKKAAKK 29
; TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acide
TYPE: amino acid
STRANDEDNESS: N/A
                                                                                                                                                         Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.7
Best Local Similarity 62.1
Matches 18; Conservative
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PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                    Best Local Similarity
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                                                                                                               Query Match
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5.1.3
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
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protein search, using sw model OM protein - March 10, 2003, 12:15:04 ; Search time 13.1962 Seconds (without alignments) 327.825 Million cell updates/sec Run on:

US-09-816-989A-2 213 1 AKKYAKKAKAEKAKKAYKAA......AKYEKAAAEKAAAKEAAYEA 45 Title: Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

283224

length: 0 length: 200000000 DB seq DB seq Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	histone H1 - sea u	membrane spanning	membrane spanning	tolA protein - Esc	ď		sperm tail-specifi	histone H1-beta, e	probable hupB - My	DNA topoisomerase	outer membrane pro	hypothetical prote	mst101-1 protein -	Tola protein PA097	histone H1 homolog	histone H1, gonada	1-acylglycerol-3-p	asparaginyl-trna s	hypothetical prote	_	probable zuotin [i	probable DNA topoi		histone H1 - rainb	hypothetical prote	histone H1-gamma,	hypothetical prote	cgcr-1 protein - C	histone H1 - midge
	ID	A25550	F90725	G85576	JV0057	AE1317	AE1689	S51364	A28100	G70673	B87553	B43592	F70742	834153	E83525	861926	HSUR1P	T35503	T39675	T17698	T34625	T50972	T36664	HSTR1	HSTRIR	AB1487	A26721	T30977	S19114	S40436
	Query Match Length DB	1	394 2			239 2					899 2																			
<b>%</b>	Match	48.6	46.0		46.0	44.4	42.3	42.3	42.0	42.0	41.3	40.6	40.4	40.4	٥.			ω.	38.5	•	٠	•		•	37.6	37.6	37.3	37.1	37.1	37.1
	Score	103.5		. 86	98	94.5	90	90		89.5	88	86.5	98	98	98	82	82	82	82	81.5	80.5		80.5	80	80	80	79.5	79		79
1	No.	-	7	m	4	ß	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27		53

probable rotamase	histone H1 - Chlam	histone H1 - tomat	polyhydroxyalkanoa	tolA protein [impo	histone H1.10 - ch	histone H1-5 [vali	invariant surface	probable transfera	histone HIA - Afri	histone H1-II - Vo	Tola colicin impor	ribosomal protein	hypothetical prote	histone H1 - mouse
A81794	S59589	845662	G83013	AG0592	A28456	S51660	B38145	B70868	151227	JN0748	AC0138	JC5954	T06636	A28470
01 0	N (1	N	N	N	N	Н	N	N	~	N	N	0	~	N
347	231	287	309	376	220	226	523	580	229	241	388	220	924	212
37.1	36.6	36.6	36.6							35.7	35.7	35.4	35.4	35.2
79 37.1	78 36.6	78 36.6	78 36.6			77 36.2				76 35.7	76 35.7	75.5 35.4		

#### ALIGNMENTS

histone H1 - sea urchin (Lytechinus pictus) C,Species: Lytechinus pictus (painted urchin) C,Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 23-Jul-1999

C;Accession: A25550
R;Knowles, J.A.; Childs, G.J.
Nucleic Acids Res. 14, 8121-813, 1986
A;Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus and A;Reference number: A25550; MUID:87040778; PMID:3022245

A;Molecule type: DNA A;Residues: 1-210 <KNO> A;Cross-references: GB:XO4488; NID:g9616; PIDN:CAA28177.1; PID:g9617 C;Superfamily: histone H1 C;Superfamily: histone H1 C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus

Gaps .; Length 210; Indels Score 103.5; DB 2; Pred. No. 0.0053; 3; Mismatches 48.6%; Query Match
Best Local Similarity 65.13
Matches 28; Conservative

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166 AKKAAKKPAAKKPAKKAAKKPAAKKAAKPAAKKAAKAA 208 1 AKKYAKKAKAEK-AKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42 셤 ઠે

RESULT 2

membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain i C; Species: Escherichia coli
B; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G., Syasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
BNA Res. 9, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genor A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: F90725
A; Molecule type: DNA

A;Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:gl3360233; GSPDB:GN00154 A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics: A;Gene: RC80774 A;Residues: 1-394 <HAY>

Gaps ; 9 Query Match
46.0%; Score 98; DB 2; Length 394;
Best Local Similarity 65.3%; Pred. No. 0.028;
Matches 32; Conservative 2; Mismatches 9; Indels

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Abjoint ical protein lmo1941 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Species: Abov-2001
C;Accession: AE1317
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
D; Jones, L.M.; Karst, U.
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Tutle: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Accession: AE1317
A;Status: preliminary
A;Accession: AE1317
A;Status: preliminary
A;Cross-references: GB:NC_003210; PIDN:CAD00019.1; PID:gl6411394; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cibecies: Listeria innocua
Cibace: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
CiAccesion: AE1689
Cidaces: P: Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
Cidaces: Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Cidacc. 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoce, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: GB:AL592022, PIDN:CAC97285.1, PID:g16414556, GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 94.5; DB 2; Length 239;
Pred. No. 0.04;
7; Mismatches 9; Indels
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Pred. No. 0.11;
3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 KAAAEKAEADKKKOEEDAVKAANAKKEQEAAEEKAAADKAAAEKAAAE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 KKAAEKAAAEKAAAEKAAAEKAAADKKAAA-AKAAAEKAAAAEA
  1 AKKYA-KKAKAEKAKKAYKAAEAKKA
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il Similarity 56.2%;
27; Conservative 7
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1 Similarity 45.5%;
30; Conservative 3
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Best Local Similarity
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Best Local Similarity
Matches 27; Conserva
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A;Molecule type: DNA
A;Residues: 1-243 <GLA>
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                                                                                                                                 A Molecule type: DNA
A, Residues: 1-421 < Lab.
A, Robertmental source: strain JM105
A, Note: the authors translated the initiation codon GTG for residue 1 as Val
A, Note: the authors translated the initiation codon GTG for residue 1 as Val
R, Blattner, F.R.; Plumkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A, Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A,Title: The complete genome sequence of Escherichia coli K-12.
A, Reference number: A64720; MUID:97426617; PMID:9278503
A, Accession: B64810
A, Accession: acid sequence not shown; translation not shown
A, Molecule type: DNA
A, Residues: 1-421 < BLAT>
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ClolA protein - Escherichia coli (strain K-12)

C;Species: Bscherichia coli

C;Species: Bscherichia coli

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002

B;Levengood, S.K.; Webster, R.E.

J. Bacteriol. 171, 6600-6609, 1989

J. Bacteriol. 171, 6600-6609, 1989

A;Title: Nucleotide sequences of the tolA and tolB genes and localization of their produ

A;Reference number: JV0057; MUID:90078104; PMID:2687247
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C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t
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  KKAAEKAAAEKAAADKKAAAEKAAADKKAAA-AKAAAEKAAAAKAAAEA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 KKAAEKAAAEKAAADKKAAAEKAAADKKAAA-AKAAAEKAAARAAAEA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 394;
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larity 65.3%; Pred. No. 0.029;
Conservative 2; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;14-34/Domain: transmembrane #status predicted <MSS>F;78-301/Domain: helical #status predicted <HSR>F;355-362/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 98; DB 2;
Pred. No. 0.028;
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Best Local Simi
Matchep 32;
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Gaps

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-AKYEKAAAEKAAA 38

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Cjaccession: B87553
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon,
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A, Accession: G70673
A, Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-214 <COLD.
A, Residues: 1-214 <COLD.
A, Cross-references: GB:Z83018; GB:AL123456; NID:g3261671; PIDN:CAB05427.1; PID:g1694845
A, Experimental source: strain H37Rv
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C;Date: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 08-Oct-1999
C;Accession: B43592
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A,Cross-references: GB:MS8563; NID:g155066; PIDN:AAA27480.1; PID:g155067
A,Note: the authors translated the codon TTC for residue 316 as Tyr, and C,Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 89.5; DB 2; Length 214; Pred. No. 0.11; 4; Mismatches 13; Indels
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40.6%; Score 86.5; DB 2;
Best Local Similarity 54.5%; Pred. No. 0.32;
Matches 24; Conservative 6; Mismatches 13;
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5; Mismatches
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Best Local Similarity 55.6%;
Matches 25; Conservative
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A,Gene: hupB
C;Superfamily: histone H1
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A,Status: preliminary
A,Molecule type: DNA
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Matches
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histone H1-beta, embryonic - sea urchin (Strongylocentrotus purpuratus)
histone H1-beta, embryonic - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 23-Feb-1997
C;Accession: A28100
R;Lai, Z.C.; Childs, G.
Mol. Cell. Biol. 8, 1842-1844, 1988
A;Title: Characterization of the structure and transcriptional patterns of the gene enco
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                                                                            Species: Drosophila hydei
C;Species: Drosophila hydei
C;Accession: S51364; S34154
R;Neesen, J:; Padmanabhan, S.; Buenemann, H.
Eur. J: Blochem. 225, 1089-1085, 1994
A;Title: Tandemly arranged repeats of anovel highly charged 16-amino-acid motif represible harmoner s51364; MUID:95045538; PMID:7957199
A;Reference number: S51364; MUID:95045538; PMID:7957199
A;Accession: S51364
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1390 «NEE>
A;Cross references: EMBL:X73481
R;Messen, J:; Heinlein, U.A.O.; Buenemann, H.
S;Messen, J:; Heinlein, U.A.O.; Buenemann, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable hups - Mycobacterium tuberculosis (strain H37RV)
[Species: Mycobacterium tuberculosis
[Species: Mycobacterium tuberculosis
[Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
[Spacession: G70673
[Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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[Species: 17. Jul-1998 #text_change 20-Jul-1998 #text_change 20-Jul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-163,'E',164-236,'Q','237-254,257-320,'E',321-1390 <NEW>
A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
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C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; embryo; nucleosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.3%; Score 90; DB 2; Length 1390;
57.8%; Pred. No. 0.41;
ive 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 89.5; DB 2; Length 2
Pred. No. 0.11;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               662 KETAEKKKCEKAAKKRKEAAEKKKCAEAAKKEKEAAEKKKCEEAA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 SKKTTKKVKKPAAKKAKPA-AKKAAK--KPAAKKPAAKKAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: FlyBase: FBgn0011816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.0%;
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Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Conservative
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A;Molecule type: DNA
A;Residues: 1-211 <LAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Gene: mst101(2)
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Gaps

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Search completed: March 10, 2003, 12:28:26 Job time : 14:1962 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 'X',3-39 <SCA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Gene: bpHl
C, Superfamily: histone H1
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                                                                                                                                                                                                           hypothetical protein Rv0475 - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Accession: F70742
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tola protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.;; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-199 <COL>
A;Experimental source: GB:Z77162; GB:AL123456; NID:G3261606; PIDN:CAB00936.1; PID:e255021;
A;Experimental source: strain H37RV
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S34153
mst101-1 protein - fruit fly (Drosophila hydei)
mst101-1 protein - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34153
R;Nesesen, J.; Heinlein, U.A.O.; Buenemann, H.
R;Nesesen, J.; Heinlein, U.A.O.; Buenemann, H.
A;Reference number: S34153
A;Reference number: S34153
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-344 <NES>
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40.4%; Score 86; DB 2; Length 344;
Best Local Similarity 57.8%; Pred. No. 0.33;
Matches 26; Conservative 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels
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                                    1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: X73480; NID: 9313199; PID: 9313200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
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A;Gene: FlyBase:Dhyd/mst101
A;Cross-references: FlyBase:FBgn0011816
C;Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 EKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: Rv0475
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A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho-A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83525
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-347 <STO>
A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001:A;Experimental source: strain PA01
A;Experimental source: strain PA01
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Scarlato, V.; Arico, B.; Goyard, S.; Ricci, S.; Manetti, R.; Prugnola, A.; Manetti, R., Mol. Microbiol. 15, 871-881, 1995
A;Title: A novel chromatin-forming histone H1 homologue is encoded by a dispensable and ci. A;Reference number: S61926; MUID:95319329; PMID:7596289
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histone H1 homolog - Bordetella pertussis
histone H2 Bordetella pertussis
C;Species: Bordetella pertussis
C;Date: 23-Jul-1996 #sequence_revision 06-Sep-1996 #text_change 24-Nov-1999
C;Accession: S61926; S69327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-182 <SCA1>
A;Cross-teferences: BMBL:L37438; NID:g777717; PIDN:AAB59120.1; PID:g777718
A;Accession: S69327
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                                                                                                                                                                                                                                                                                                                                                      Query Match 40.4%; Score 86; DB 2; Length 347; Best Local Similarity 51.1%; Pred. No. 0.33; Matches 24; Conservative 6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.9%; Score 85; DB 2; Length 182;
61.4%; Pred. No. 0.25;
tive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 406, 959-964, 2000
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 10, 2003, 12:15:01 ; Search time 10.2532 Seconds
 (without alignments)
182.035 Million cell updates/sec

US-09-816-989A-2 213 1 AKKYAKKAKABKAKKAYKAA......AKYEKAAAEKAAAKEAAYEA 45 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P06144 lytechinus	_	Q08696 drosophila	-	P15869 strongyloce	_	P29720 treponema p	-	_	P50600 pseudomonas	Q9xb18 mycobacteri		-						P40278 chironomus			-							Q08865 volvox cart	Q9rq15 bacteroides		_	Q93mh6 enterobacte
SUMMARIES	ID		TOLA ECOLI	MST2_DROHY		H1B_STRPU	DBH_MYCTU	TMPB TREPH	HBHA MYCTU	MST1_DROHY	TOLA PSEAE	DBH_MYCBO	H1 PARAN	H1E CHIPA	TOP1 STRCO	H1_SALTR	H1_ONCMY	H1G_STRPU	H10_CHITH	HIE CHITE	H11 GLYSA	H1_LYCES	RL22_DROME	H110_CHICK	H15_HUMAN	ASR_KLEPN	H12_GLYBA		H1_WHEAT	H12_VOLCA	RS16_BACTN			ASR_ENTCL
	038	-	٦	٦	7		Н	٦	Н	ч	Н	Н	-	Н	-	Н	П	-	Н	~	н	Н	П	Н	П	Н	ч	Н	7	Н	7	<del>,-1</del>	-	Н
	Query Match Length	210	421	1391	208	211	214	384	198	344	347	205	248	235	952	194	206	217	244	237	233	287	299	219	225	139	232	233	238	240	184		211	101
dł	Query Match	48.6		42.3	42.0	42.0	42.0	40.6	40.4	40.4	40.4	40.1	38.5	38.0	37.8	37.6				ė.	36.6	36.6	36.4	•	36.2	2	35.9	S.	35.9	35.7	35.4	35.4	35.2	35.0
	Score	103.5	98	an a		89.5	89.5	86.5	98	86	86	85.5	82	81	80.5	80	m	79.5	79	78.5	78	78	77.5	77	77	76.5	76.5	76.5	76.5	9/	S	75.5	75	74.5
	Result No.	п	~	m	4	Ŋ	9	7	<b>6</b> 0	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P58122 caulobacter P39730 saccharomyc	P15276 pseudomonas P5056s chlamydomon P15796 caenorhabdi	P43277 mus musculu P09426 anas platyr P44678 haemophilus	Q23858 dictyosteli O86537 streptomyce P08288 gallus gall
RS16_CAUCR IF2P_YEAST	ALGP_PSEAE H2B1_CHLRE H12_CAEEL	H13 MOUSE H1 ANAPL TOLA HAEIN	CRTC_DICDI DBH2_STRCO H11R_CHICK
п п			444
165 1002	352 153 190	220 217 372	424 218 218
35.0	34.7	34.0	34.0 33.8 8.8
74.5	74 73 73	73 72.5 72.5	72.5 72 72
3.4 3.5	36 38 38	4 4 4 0 1 2	4 4 4 6 4 8

## ALIGNMENTS

RESULT 1

H1 1	H1 LYTPI
'n	H1 LYTPI STANDARD; PRT; 210 AA.
AC	•
ΤΩ	988 (Rel.
DŢ	(Rel.
υŢ	. 38, Last
OE	Late histone H1.
SO	Lytechinus pictus (Painted sea urchin).
ဗ	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
ဗ	Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
ပ္ပ	Lytechinus.
ŏ	NČBI TaxID=7653;
RN	_ [t]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RX	MEDLINE=87040778; PubMed=3022245;
RA	Knowles J.A., Childs G.J.;
RT	"Comparison of the late H1 histone genes of the sea urchins
RŢ	Lytechinus pictus and Strongelocentrotus purpuratus.";
RL	Nucleic Acids Res. 14:8121-8133(1986).
ນ	>
ပ္ပ	NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
ပ္ပ	
ပ္ပ	"-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
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ပ္ပ	entities requires a license agreement (See http://www.isb-sib.ch/announce/
ပ္ပ	or send an email to license@isb-sib.ch).
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DR	EMBL; X04488; CAA28177.1;
DR.	PIR; A25550; A25550.
DR	HSSP; P02259; 1HST.
DR	InterPro; IPR001386; Histone H1/H5.
DR	InterPro; IPR003216; Linkerhiet N.
В	Pfam: PF00538; linker histone; 1.
DR	ProDom; PD000373; Linkerhist N; 1.
DR	SMART; SM00526; H15; 1.
Ž	Chromosomal protein; Nuclear protein; DNA-binding; Multiqene family.
δS	SEQUENCE 210 AA; 21746 MW; 08C38F64894007E2 CRC64;
õ	1 48.6%;
Be	cal Similarity 65.1%; Pred. No. 0.0016;
Ma	Matches 28; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

g ઠ

RESULT 2 TOLA\_ECOLI

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                                                                                                                                                                                                                                           Levengood S.K., Webster R.E.; "Nucleotide sequences of the tolA and tolB genes and localization of their products, components of a multistep translocation system in Becherichia coli."; J. Bacteriol. 171:6600-6609(1989).
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97426617; PubMed=9278503; MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99332679; PubMed=10404600; MEDLINE=99332679; PubMed=10404600; MEDLINE=99332679; PubMed=10404600; MEDLINE=99332679; PubMed=10404600; Michael J., Hennecke F., Plueckthun A., Wlodawer A.; Elidowentous phage infection: crystal structure of g3p in complex with its coreceptor, the C-terminal domain of TolA."; Structure 7:711-722(1999).
-!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A COLICING (COLICING A. E1, E2, E3, AND K). NECESSARY FOR THE COLICING TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97133271; PubMed-8978668;
Derouiche R., Gavioli M., Benedetti H., Prilipov A., Lazdunski C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91296736; PubMed=2068069; Levengood S.K., Beyer W.F. Jr., Webster R.E.; TrolA: a membrane protein involved in colicin uptake contains an excended halical region."; Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(1991).
                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "TolA central domain interacts with Escherichia coli porins.";
EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                               01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
   421 AA
                                                                                TolA protein.
TOLA OR CIM OR EXCC OR LKY OR B0739.
Escherichia coli.
                                                                                                                                                                                                                            MEDLINE=90078104; PubMed=2687247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97061202; PubMed=8905232;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERACTION WITH PORINS.
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gregor J., Davis
Mau B., Shao Y.;
                                                                                                                                                                NCBI_TaxID=562;
                                 01-FEB-1991
01-FEB-1991
                                                                                                                                               Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             loubes R.;
   TOLA ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAINS
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SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE AND LAMB.
-!- SCHCELLULAR LOCATION: Type II membrane protein. Inner membrane.

OF BACTERIOPHAGE DNA.

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ب
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DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                     EMBL; M28232; AAA24683.1; -.
EMBL, AE00017; AAC73833.1; -.
EMBL, D90713; BAA35405.1; -.
PIR; JV0057; JV0057.
PDB; JTOL; 20.MAX-99.
ECGGene; EG11007; tolA.
Transport; Protein transport; Bacteriocin transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95045538; PubMed=7957199;
MEDLINE=95045538; PubMed=7957199;
Neesen J., Padmanabhan S., Buenemann H.;
Neesen J., Padmanabhan S., Buenemann H.;
Neesen J., Padmanabhan S., Buenemann H.;
Menti representing the major component of the sperm-tail-specific axoneme-associated protein family Dhmstl01 form extended alpha-helical rods within the extremely elongated spermatozoa of Drosophila hydel.",
Bur. J. Blochem. 225:1089-1095(1994).
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL.
-!- SUBCELLULAR LOCATION: Cytoplaemic.
-!- TISSUE SPECIFICITY: TESTIS. PRIMARY SPERMATOCYTES AND EARLY
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 98; DB 1; Length 421;
Pred. No. 0.0097;
2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 KKAAEKAAAEKAAADKKAAAEKAAADKKAAA-AKAAAEKAAAAKAAAEA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat; Inner membrane; 3D-structure; Complete proteome.

1 13 CYTOPLASMIC (POTENTIAL).

TRANSMEM 14 34 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8B2F52B4B97C655E CRC64;
                                                                                                                                                                                                                                                                                                                                                                            PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Axoneme-associated protein mst101(2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AA; 43156 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 65.3
32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                 13
421
310
421
278
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35
48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MST101(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        008696;
                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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211 AA.

or send an email to license@igb-sib.ch)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=88246461; PubMed=2837660;
Lai Z.-C., Childs G.
Characterization of the structure and transcriptional patterns of the gene encoding the late histone subtype HI-beta of the sea urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp) (21-kDa laminin-2-binding protein).
HUP OR HLP OR LBP21 OR RV2986C OR MT3064 OR MTCY349.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Mycobacterineae; Mycobacteriam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strongylocentrotus purpuratus.";
Mol. Cell. Biol. 8:1842-1844(1988).
-!- FUNCTION: HISTONES H1 ARB NECESSARY FOR THE CONDENSATION OF NUCLECOOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 42.0%; Score 89.5; DB 1; Length 211; Best Local Similarity 61.9%; Pred. No. 0.034; Matches 26; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 SKKTTKKVKKPAAKKAKKPA-AKKAAK--KPAAKKPAAKKAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42
                                                                                                                                                                     01-APR-1990 (Rel. 14, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Histone H1-beta, late embryonic.
                                                                                                                                      01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M20314; AAA30052.1; -.
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                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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STRAIN=H37Rv;
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                                                                     H1B STRPU
P15869;
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      RESULT 5
HIB_STRPU
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DBH MYCTU
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                                                                                                       SON SENSO SE
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                                                          Flybase; FBgn0020733; Dhyd\mst101(2).
Sperm; Repeat; Multigene family; Polymorphism.
DOWAIN 332 1268 59 x 16 AA APPROXIMATE TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. Gen. Genet. 260:475-479(1998).
FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STAINA-ATCC 700084 / mc(2)155;
MEDLINE=99110.209; PubMed=9894918;
Lee B.H., Murugasu-Oei B., Dick T.;
"Upregulation of a histone-like protein in dormant Mycobacterium
                                                                                                                                                                     [KR]-K-X-C-X-X-X-A-K-X-K-X-K-X-X-E. 1391 AA; 159000 MW; 1B2A368F30F48878 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSZHCS;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKKYAKKAKAEKA-----KKAYKAAEAKKAAKY--EKAAAEKAAKEAAYEA
                                                                                                                                                                                                                                                                         DB 1; Length 1391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIAL HISTONE-LIKE DOMAIN.
DEGENERATE REPEATS REGION.
CASF577F61F7EF09 CRC64;
                                                                                                                                                                                                                                                                                                                                        11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    663 KETAEKKKCEKAAKKRKEAAEKKKCAEAAKKEKEAAEKKKCEEAA 707
                                                                                                                                                                                                                                                                                                                                                                                                      42.0%; Score 89.5; DB 1
53.7%; Pred. No. 0.033;
                                                                                                                                                                                                                                                                   42.3%; Score 90; DB 1;
57.8%; Pred. No. 0.15;
cive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000119; Bac_DNAbind.
Pfam; PF00216; Bac_DNA binding; 1.
Probom; PD000945; Bac_DNAbind; 1.
SMART; SM00411; BHL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00045; HISTONE LIKE; 1
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HSSP; P02346; 1HUU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21230 MW;
EMBL; X73481; CAA51876.1; -.
                                                                                                                                                                                                                                                                                                     Local Similarity 57.8
les 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium smegmatis.
                                     PIR; S34154; S34154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Local Sim.
29;
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1D DBH MACSM

1D DBH MACSM

10-0C

DT 16-0C

DT 16-0C

DE DNA-DOMAIL

10-0C

OC Actin

OC Actin
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Gaps

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214 AA.

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                                                                                                                                                                                                  Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell F., Sliviensky L., Schouls L., van Embden J.D., Charon N.W.; "Treponema phagedenis encodes and expresses homologs of the Treponema pallidum TmpA and TmpB proceins."; pallidum TmpA and TmpB proceins."; Infect. Immun. 59:3685-3693(1991).

-i. FUNCTION: TMP MAY SERVE AS A PORIN OR TRANSPORT PROTEIN FOR LARGE MOLECULES.
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Treponemal membrane protein B precursor (Antigen tmpB).
                                                                                Treponema phagedenis.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
NGI TaxID=162;

    SUBCELLULAR LOCATION: OUTER MEMBRANE-ASSOCIATED.
    SIMILARITY: TO TMPB OF T.PALLIDUM.

                                                                                                                                                                            STRAIN=Kazan 5;
MEDLINE=91372983; PubMed=1894368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M58563; AAA27480.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B43592; B43592
                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh,
Fleistchmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleistchmann R.D., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salaberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Savita P.;
Submitted (DEC-1997) to the SWISS-PROT data bank.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC UNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                     Harris D.
            Gordon S.T., Brosch, R., Parkhill J., Garnier T., Churcher C., Harris D. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Peltwell T., Gentles S., Hamin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Squares S., Squares R., Torciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tubercuist;
Tuberco; TeR00019; Bac DNAbind;
Tefam; Pro0524; HISTONEHS.
PRINTS; PR00624; HISTONEHS.
PROSITE; PS000045; Bac DNAbind; 1.
SWART; SW00041; BHL; I.
PROSITE; PS000045; HISTONE LIKE; 1.
PROSITE; PS000045; HISTONE LIKE; 1.
PROSITE; PS000045; Bac DNAbind; Repeat; Complete protecome.
DOMAIN 10 DOMAIN.
DOMAIN 10 DEGENERATE REPEATS RECTON.
SEQUENCE 214 AA; 22187 MW; CB09AF20FB353544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prasad H.K., Annapurna P.S., Dey A.B., Tyagi J.S., Jain N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ',
0.034;
~hea 13; Indels
                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.0%; Score 89.5; DB 1;
55.6%; Pred. No. 0.034;
cive 4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 71-86, AND DNA-BINDING.
 MEDLINE=98295987; Pubmed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AE007127; ARK47393.1; -. HSSP, P02346; 1HUU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z83018; CAB05427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-H37Rv;
                                                                                                                                                                                                                                                                                                                                     Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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POTENTIAL. TREPONEMAL MEMBRANE PROTEIN B. 17 X 5 AA TANDEM REPEATS OF K-A-A-[AKR]-[ED].

membrane; Repeat; Signal.

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                                                                AA TANDEM REPEATS OF [EA]-A-A-R-X-
                                                                                                                                                                                Gaps
                                                                                                                                                                                1;
                                                                                                                                                             40.6%; Score 86.5; DB 1; Length 384;
                                                                                                                                                                               13; Indels
                                                                                                                                          6E94CBC74294DE8C CRC64;
                                                                                                                                                                                                             1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYE 44
                                                                                                                                                                      Pred. No. 0.11; 6; Mismatches
                                                        1-17.
6 X 8 .
A-A-E.
-11.
                                                                                                                                           42677 MW;
                                                                                                                                                                     54.5%;
                                                                                                                                                                                24; Conservative
                                                                                  236
245
254
263
272
281
384 AA;
                                                                                                                                                                      Local Similarity
                                                                                                                                 REPEAT
SEQUENCE
                                                                                                                                                              Query Match
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1 AKKYAKKAKAKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45

25; Conservative

Matches

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384 AA

STANDARD;

RESULT 7 TMPB\_TREPH ID TMPB\_TREPH AC P29720;

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Nature 412:190-194 (2001).
-!- FUNCTION: REQUIRED FOR EXTRAPULMONARY DISSEMINATION. MEDIATES
ADHERENCE TO REITHELIAL CELLS BY BINDING TO SULFATED
GLYCOCONJUGATES PRESENT AT THE SURRACE OF THESE CELLS; BINDS
HEPARIN, DEXTRAN SULFATE, FUCCIDAN AND CHONDROITIN SULFATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=M.tuberculosis, STRAIN=CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey B.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                    SPECISES-M. tuberculosis; STRAIN=H37RV;
MEDLINE=98259597; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Roghwall T., Gentles S., Hamiln N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Woule S., Murphy L.,
Oliver S., Geborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                Bacteria, Actinobacteria, Actinobacteria (class), Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.NCBI_TaxID=1773, 1765,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
SPECIES-Mutuberculosis, and M.bovis;
STRAIN-H37RV, ATCC 201 / H37Ra, and BCG / Paris 1173 P2;
MEDLINE-98445421; Pubmed-9770536;
Menozzi P.D., Bischoff R., Fort E., Brennan M.J., Locht C.;
Molecular characterization of the mycobacterial heparin-binding hemagglutinin, a mycobacterial adhesin.";
Proc. Natl. Acad. Sci. U.S.A. 95:12625-12630(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=103, and BCG;
MEDILIBE=21342355; PubMed=11449276;
Pethe K., Alonso S., Biet F., Delogu G., Brennan M.J., Locht C.,
Menozzi F.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Menozzi F.D., Rouse J.H., Alavi M., Laude-Sharp M., Muller J., Bischoff R., Brennan M.J., Locht C., Identification of a heparin-binding hemagglutinin present in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-16, AND CHARACTERIZATION.
SPECIES—W tuberculosis, and M. bovis;
STRALN-ATCC 201 / H37Ra, and BCG / Paris 1173 P2;
MEDLINE-97188915; PubMed=9064359;
                                            011142; 085733;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Heparin-binding hemagglutinin (Adhesin).
HBHA OR RV0475 OR WT0493 OR WTCY20G9.01.
                                 198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=M.tuberculosis, and M.bovis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exp. Med. 184:993-1001(1996).
                                                                                                                                                  Mycobacterium tuberculosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 393:537-544(1998).
                               STANDARD;
                                                                                                                                                                     Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                               MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bishai W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                              MISCELLANEOUS: SERUM FROM PATIENTS DIAGNOSED WITH ACTIVE TUBERCULOSIS THAT HAD NOT BEEN VACCINATED CONTAINS ANTIBODIES THAT RECOGNIZE HBHA, WHEREAS SERUM FROM HEALTHY INDIVIDUALS DOES NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94200512; PubMed=8150205;
Neesen J., Buenemann H., Heinlein U.A.;
Neesen J., Buenemann H., Heinlein U.A.;
"The Drosophila hydei gene Dhmstl01(1) encodes a testis-specific,
"The Drosophila hydei gene Dhmstl01(1) encodes a testis-specific,
repetitive, axoneme-associated protein with differential abundance in
Y chromosomal deletion mutant flies.";
Dev. Biol. 162:414-425(1994).
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL. IT IS
ASSOCIATED WITH AXONEMAL STRUCTURES.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUE SPECIFICITY: TESTIS. LOCATED IN SPERMATOCYTES AND
PROMOTES HEMAGGLUTINATION OF ERYTHROCYTES OF CERTAIN HOST SPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophija hydei (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Ilnsecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                      DOMAIN OF HEHA. PROGRESSIVE TRUNCATIONS FROM THE C-TERMINAL END DIMINISH THE APPINITY FOR HEPARIN.

PTM: GLYCOSYLATED. GLYCOSYLATION MAY PROTECT THE PROTEIN FROM PROTECLYTIC DERADATION AND BE IMPORTANT FOR HEMAGGLUTINATION. IN SUGGESTS THAT THE CARBOHYDRATE MOIETY MAY BE LOCATED WITHIN THE TERMINAL DOMAIN OF HEHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z77162; CAB00936.1; -.
EMBL; AE06951; AAK44716.1; ALT_INIT.
TIGR; MT0493; -.
Tuberculist; Rv0475; -.
Cell adhesion; Heparin-binding; Hemagglutinin; Glycoprotein;
Virtlence; Complete proteome.
                        INDUCES MYCOBACTERIAL AGGRECATION.
SUBCELLULAR LOCATION: SURFACE ASSOCIATED.
DOMAIN: HEPARIN BINDING SEEMS TO REQUIRE THE C-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.4%; Score 86; DB 1; Length 198; ilarity 65.6%; Pred. No. 0.068; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 ALA/LYS-RICH.
120 R -> P (IN REF. 1).
21403 MW; 513760F6F1EB6042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -! - SIMILARITY: STRONG, TO M.LEPRAE HBHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 EKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Axoneme-associated protein mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF074390; AAC26052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPERMATID BUNDLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MST1_DROHY
Q08695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MST101(1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
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the European Bioinformatics Institute.
                                                                                                                                                                                                                        Local Similarity
es 24; Conserv
                                                                                                                     Complete proteome. DOMAIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=AN5;
                                                                                                                                            TRANSMEM
                                                                                                                                                                                                              Query Match
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                               RESULT 11
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                                                                                                                                                                                                                                                                             ;
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                 Sperm, Repeat; Multigene family.
DOMAIN 58 337 19 X 16 AA APPROXIMATE TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
WEDLINE-20437337; Pubmed-10984043;
KEDLINE-20437337; Pubmed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody I.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Raizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                                                                            K-K-K-C-X-E-X-A-[KQ]-K-X-X-E-X-A-X. 344 AA; 37793 MW; 24C65D2510387E2A CRC64;
  -!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELLCAL.
-!- POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN STRAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                               Score 86; DB 1; Length 344;
Pred. No. 0.11;
3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dennis J.J., Lafontaine E.R., Sokol P.A.; Infontation and characterization of the tolQRA genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                              117 KEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAA 161
                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               347 AA
                                                                                                                                           EMBL; X73480; CAA51875.1; -.
PIR; S34153; S34153.
FlyBase; FBgn0011816; Dhyd\mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97113525; PubMed=8955385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996)
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.8%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              opportunistic pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS TO N-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOLA OR PA0971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tola protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=PAO;
                                                                                                                                                                                                                                                                                                                                                                                               PSEAE
                                                                                                                                                                                                                          SEQUENCE
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                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PROVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prabhakar S., Tyagi J.S., Prasad H.K.; "HLPMt-A target for differentiation of M.tuberculosis and M.bovis."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                     EMBL; AE004530; AAG04360.1; -.
Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBL_TaxID=1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BCG / Tokyo;
Matsumoto S., Yukitake H., Matsuo T., Mineda T., Yamada T.;
"Identification of a novel protein generating bacterial slow growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
7
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Q9XB18; Q9S5J5;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp)
HUP OR HLP OR MDP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.4%; Score 86; DB 1; Length 347; llarity 51.1%; Pred. No. 0.11; Conservative 6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from Mycobacterium.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                           1 16 CYTOPLASMIC (POTENTIAL).
17 37 POTENTIAL.
38 347 PERIPLASMIC (POTENTIAL).
209 216 POLY-ALA.
347 AA, 37935 MW; EEDD4B04AA095945 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB013441; BAA78330.1; -.
HSSP; P02346; 1HUU.
InterPro; IPR000119; Bac DNAbind.
InterPro; IPR001386; Histone_H1/H5.
Pfam; PR00216; Bac DNA binding; 1.
PRINTS; PR00624; HISTONEHS.
ProDom; PD000945; Bac_DNAbind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y18421; CAB46493.1; -.
                                                                                                                                                                                                                                EMBL; U39558; AAC44660.2; -. EMBL; AE004530; AAG04360.1;
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[1]
SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=7151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1902;
                                                                     01-FEB-1995 (
01-FEB-1995 (
15-JUL-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 KKA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces
                                                                                                         Histone H1E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 YEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRCO
                                                CHIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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09X909,
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Strickland W.N., Strickland M., Brandt W.F., von Holt C., Lehmann A.,
Wittmann-Liebold B.;
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    "The primary structure of histone H1 from sperm of the sea urchin
Parechinus angulosus. 1. Chemical and enzymatic fragmentation of the
protein and the sequence of amino acids in the four N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 2. Sequence of the C-terminal CNBr peptide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the entire primary structure.";

Eur. J. Biochem. 104:567-578(1980).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: SPERM.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                               DB 1; Length 205;
                                  90 BACTERIAL HISTONE-LIKE DOMAIN.
205 DEGENERATE REPEATS REGION.
1199 A -> T (IN REF. 2).
21262 MW, 19FCEG7885DFE648 CRC64;
                                                                                                                                                                                                                                                                                                  Parechinus angulosus (Angulate sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=80156831; PubMed=6767609;
Strickland W.N., Strickland M., de Groot P.C., von Holt C.,
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 248;
                                                                                                                     12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 144 K -> R.
248 AA; 26387 MW; 1B25B3F136541947 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 KKAKKTSAAAKAKA-KAAAKKARKAKAAAKKKAALAKKKAAAA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAA-AKEAAYEA 45
                                                                                                                                                                  111 AKKVAKKAPAKKATKAAKKAATKAPA---KKAATKAPAKKA 148
                                                                                                                                          1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEA 41
                                                                                             40.1%; Score 85.5; DB 1
58.5%; Pred. No. 0.078;
cive 2; Mismatches 1
                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.5%; Score 82; DB 1
57.8%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
SMART; SM00411; BHL; 1.
PROSITE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cyanogen bromide peptides.";
Eur. J. Biochem. 104:559-566(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist N.
Pfam; PF00538; linker histone; I.
ProDom; PD000373; Linkerhist N; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Conservative
                                                                                                                     24; Conservative
                                                                                                                                                                                                                              STANDARD;
                                               205
199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00526; H15; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A02586; HSURIP.
HSSP; P02259; 1HST.
                                                                                                                                                                                                                                                                                       Histone H1, gonadal.
                                             101
199
105 AA;
                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 80-248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-84.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7658;
                                                                                                                                                                                                                                                                                                                                       Parechinus
                                                          CONFLICT
                                                                                                                                                                                                                           H1_PARAN
P02256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
                                     DOMAIN
                                                DOMAIN
 STTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chironomus pallidivittatus (Midge).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Perrygota; Neoptera; Endopterygota; Diptera; Nematocera;
Chironomodea; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------KKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 235 AA; 24446 MW; 340BC5B9A85002AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA topoisomerase I EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
(Untwisting enzyme) (Swivelase).
TOPA OR SCO3543 OR SCH5.06C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schulze E., Wisniewski J.R., Nagel S., Gavenis K., Grossbach U. Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELJULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.0%; Score 81; DB 1; Length 235; 41.3%; Pred. No. 0.23; ive 2; Mismatches 17; Indels
                                                                                                          (Rel. 31, Last sequence update) (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         952 AA.
235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001386; Histone_H1/H5.
InterPro; IPR003216; Linkerhist. N.
Pfam; PP00538; linker histone; I.
ProDom; PD000373; Linkerhist_N; I.
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MEDLINE=21996410; PubMed=12000953;
                                                                    (Rel. 31, Created)
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HSSP; P08287; 1GHC.
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Conservative
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es 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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ij

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Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                    MEDLINE=78023898; PubMed=913397;
McLecd A.R., Wong N.C.W., Dixon G.H.;
McLecd A.R., Wong N.C.W., Dixon G.H.;
"The amino-acid sequence of trout-testis histone H1.";
Bur. J. Blochem. 78:281-291(1977).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SINILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
PIR; A02583; HSTR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: March 10, 2003, 12:17:08 Job time: 11.2532 secs
                                                                                                                                                                                                 InterPro; IPR001386; Histone_H1/H5. Pfam; PF00588; linker histone; 1. ProDom; PD000373; Linkerhist_N; 1. SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                        Acetylation, Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
SEQUENCE
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MOD_RES
MOD_RES
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       SEOUENCE
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         δ
                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                             Gaps
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Hopwood D.A.;
                                                                                                                                                                "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      э;
с
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InterPro; IPR003601; DNAtopi_ATP_bind.

InterPro; IPR003601; DNAtopi_DNA_Dind.

InterPro; IPR003601; DNAtopi_DNA_Dind.

InterPro; IPR003601; Prok_tpisomrase.

Pfam; PF01131; Topoisom_bac; 1.

R Fam; PF01751; Topim; 1.

R SMART; SM00413; TOPIAC; 1.

R SMART; SM00493; TOPIBC; 1.

R SMART; SM00495; TOPIBC; 1.

R SMART; SM00495; TOPIBC; 1.

R TIGRFAM; TIGR01051; topA bact; 1.

R TIGRFAM; TIGR01051; topA bact; 1.

R PROSITE; PS00396; TOPOISOMERASE I PROK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 952;
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55.6%; Pred. No. 0.86;
tive 2; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL035636; CAB38480.1; -.
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les 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygli; Neopterygli; Teleostel; Buteleostel; Protacanthopterygli; Salmoniformes; Salmonidae; Salmo.

15-JUL-1999 (Rel. 38, Last sequence update) Histone H1.

Salmo trutta (Brown trout)

RESULT 15
H1 SALTR
1D PT 21-JU
DT 21-JU
DT 15-JU
DE Histo
OS Salmo
OC Actin
OC Prota

21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last seq

STANDARD;

H1\_SALTR P02254;

888 AKKTAKKAVKKTAAKKAPAKKAAATKKTAAAKTTAAKKTAAKSTA 932

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2
                                                                 Gaps
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                                      Score 80; DB 1; Length 194; Pred. No. 0.25;
A -> I (IN MINOR COMPONENT).
D288F9F44AF9BE7E CRC64;
                                                                13; Indels
                                                                                                          105 AKKPAKKAAAPKAKKVAAKKPAAAKKPKKVAAKKAVAAKKSPKKA 149
                                                                                         41
                                                                                         37.6%; Scor.
55.6%; Pred. No. v....
            194 AA; 19408 MW;
                                                                25; Conservative
                                                   Best Local Similarity
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ACETYLATION (IN 90% OF THE CHAINS).

PHOSPHORYLATION PHOSPHORYLATION PHOSPHORYLATION

145 161 182 100

GLOBULAR.

Q9cm70 pasteurella Q23784 chironomus Q9s2m2 streptomyce

Q23784 Q9S2M2

094567 schizosacch 094528 paramecium 0911k4 enterococcu 0911k4 enterococcu 091k52 pismania 023790 chironomus 09at24 pisum sativ 09at22 pisum sativ 09at25 pisum sativ 09at25 pisum sativ 09at21 lathyrus sa 09at21 lathyrus sa 09at23 pisum sativ 09at23 pisum sativ 09at21 lathyrus sa 09at23 pisum sativ 09at23 pisum sativ 09at23 pisum sativ 09at23 pisum sativ 09at21 lathyrus sa 09at21 lathyrus sa

094567 0914528 091454 091454 0924755 0924724 0924725 0924725 0924725 0924725 0924726 0934729 0934729 0934729 0934729 0934720 0934720 0934720 0934720 0934720 0934720 0934720 0934720 0934720

Q9ndi9 plasmodium Q911h8 streptomyce Q8zqt6 salmonella Q17536 caenorhabdi

Q9NDI9 Q9L1H8 Q8ZQT6 Q17536

Q9at20 lens culina Q92em5 listeria in Q9at19 lens culina Q9rkl9 streptomyce

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SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIND 0509952;
STRAIN=0157:H7 / RIND 0509952;
STRAIN=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Schenichia coli "Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genome comparison with a laboratory strain K-12.";
DIA, Res 8. B.11-22(2001).
EMBL; AR005252; AAGS075.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Rose D.J., Maybew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grobbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potemousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                   QRX965;
QBX965;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Membrane spanning protein, required for outer membrane integrity
(Membrane spanning protein TolA).
TOLA OR 20907 OR ECS0774.
ESCherichia coll O157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
SEQUENCE FROM N.A.
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37.6
37.6
37.6
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800.5
800.5
800.8
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38X965
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Q8ajx2 streptomyce
Q92a67 listeria in
O01395 drosophila
Q9wwx1 pseudomonas
Q855f caudobacter
Q8xvn7 ralstonia s
O93946 candida alb
Q8wq44 leishmania
Q9bwy8 leishmania
Q8t9r3 leishmania
Q8t9r3 leishmania
Q81370 bordetella
Q9u33 caenorhabdi
Q9qmal ectocarpus
Q9qmal ectocarpus
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                                                          March 10, 2003, 12:15:01; Search time 23.8291 Seconds (without alignments) 389.109 Million cell updates/sec
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                                                                                                                 Description
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        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                            671580 segs, 206047115 residues
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                                           OM protein - protein search, using sw model
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Q8XVN7
Q93946
Q8WQ44
Q9BMX8
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Q8QND1
Q9AT18
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Q9AJX2
Q92A67
Q01395
Q9WWX1
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Q45370
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_bacteria:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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394 AA

PRT;

ALIGNMENTS

Taylor K.

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STRAIN=A3(2) / MA45;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Praser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL513407; CAC28545.1; -.
SEQUENCE 244 AA; 25524 MW; 61999D62CA23A7B0 CRC64;
  NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                Hopwood D.A.;
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Matches
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=EGD-E / SEROVAR 1/2A;

MEDLINE=21537279; PubMed=11679669;

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

A Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,

A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

A Domes L.-M., Kaerst U., Kreft J., Kuhn T., Hauf J., Jackson D.,

Jones L.-M., Mattournam A., Matta Vicente J., Ng E., Nadjari H.,

Nordeisek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simces N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

Comparative genomics of Listeria species.";
                                                                                                                                                              Gaps
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Pred. No. 0.053;
7; Mismatches 9; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillales,
Listeriaceae, Listeria.
                                                                                                         Score 98; DB 16; Length 394;
Pred. No. 0.04;
2; Mismatches 9; Indels
                                                                                                                                                                                                                                                 220 KKAAEKAAAEKAAADKKAAAEKAAADKKAAA-AKAAAEKAAAAKAAEA 267
                                                                                                                                                                                                         Complete proteome.
5836 MW; 72E59D576E0D7832 CRC64;
                                                                394 AA; 40517 MW; 5B58D8E8230BDE28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 294:849-852(2001).
EMBL; AL591981; CAD00019.1; -.
ListiList; LMO01941; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro, IPR002482; LysM.
Pfam; PF01476; LysM, 1.
SMART; SM00257; LysM, 1.
Hypothetical protein; Complete SEQUENCE 239 AA; 25836 MW;
                                                                                                              46.0%;
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56.28;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                          Query Match
Best Local Similarity 65.3%
....hes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative secreted protein. SCO1805 OR SCI33.04. Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 56.2
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listeria monocytogenes.
                                             Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002
01-JUN-2002
                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    Q8Y5W4 Q8Y5W4;
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(089584
100 89451
100 89451
101-M
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1D QS
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                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Deboux P.,
Entian K.-D., Fsihi H., Garcia del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Comparative genomics of Listeria species.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 akkaaeekaaaekaaeekkaaeekaadkksqedeaakaaaakkeqeaaeekaaaekaaa 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.3%; Score 90; DB 16; Length 243;
45.5%; Pred. No. 0.15;
ive 3; Mismatches 11; Indels 22;
                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
      42.7%; Score 91; DB 16; Length 244; 59.5%; Pred. No. 0.12; ive 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ll procein; Complete proteome.
243 AA; 25963 MW; 6B2493D143B159D1 CRC64;
                                                                                                                                                                                         78 SOKVAAIEAKKEAAAKKATAKKATAEKKAAAEKAAKRAAKE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Hypothetical protein lin2055.
                                                                                                                                    5 AKKAKAEKAKK--AYKAAEAKKAAKYEKAAAEKAAAKEAAYE 44
                                                                                                                                                                                                                                                                                                                                                   243 AA
                                                                                                                                                                                                                                                                                                                                                                            092A67;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MRR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                                                                                                                                                                                                                   PRT;
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STRAIN=CLIP 11262 / SEROVAR 6A;
PubMed=11679669;
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Query Match
Best Local Similarity 59.5;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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hes 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria innocua.
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23; Gaps ---AEKAA 37

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RESULT 5
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01-J0

us-09-816-989a-2.open.rspt

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A Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., A Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., A Been J., Heidelberg J.F., Alley M.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Bly B., A DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., A Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(201).

I. "Complete genome sequence of Caulobacter crescentus.", Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(201).

I. "Churersion Of One Topological Isomer Of DNA TO ANOTHER (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rodriguez-Herva J.J., Ramos J.;
"Characterization of an OprL null mutant of Pseudomonas putida.";
J. Bacteriol. 118:583-5840(1996).
EMBL; X74218; CAB50780.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.5%; Score 88.5; DB 2; Length 372; 39.7%; Pred. No. 0.31; ive 8; Mismatches 10; Indels 23
                                                           Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                        40133 MW; 87F49785ECC3C0BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DNA topolsomerase (EC 5.99.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR000380; Prok tpisomrase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; CC2451; -.
InterPro; IPR002936; DNAprim toprim.
                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001386; Histone H1/H5.
PRINTS; PR00624; HISTONEH5.
SEQUENCE 372 AA; 40133 MW; 87F4
                                                                                                                                                                                                             MEDLINE=96422022; PubMed=8824639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE005914; AAK24422.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 39.7 tes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=155892;
   FROM N.A.
                                                                                                                                                  SEQUENCE FROM N.A.
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181 AEEAKKKA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                    Axoneme-associated protein MST101(3).
MST101(3) OR DHMST101.
Drosophila hydei (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 X 16 AA APPROXIMATE TANDEM REPEATS OF X-[KQ]]-K-C-[AE]-E-X-A-[X]-K-X-X-X-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.,
"The Pseudomonas putida peptidoglycan-associated outer membrane
lipoprotein (PAL) is involved in maintenance of the integrity of the
cell envelope.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ب</u>
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Nessen J., Heinlein U.A.O., Buenemann H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-:- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
-:- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
EMBL, U88627; AAB51369.1; -.
Flybase; FBGN0020732; Dhyd\met101(3).
Sperm; Repeat; Multigene family.
DOMAIN
64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76BAA7B2A2DF732C CRC64;
                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 88.5; DB
Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 AA; 30436 MW;
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01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 61.0
nes 25; Conservative
                                                                                                                                                                                                             PRELIMINARY;
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                                  :|| |
166 DKAAKE 171
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39 KEAAYE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tola protein.
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RESULT 6

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Matches

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SEQUENCE FROM N.A.
Kaiser B., Kunkel W., Saluz H.P., Munder T.;
"Identification of Candida albicans protein domains with
transcriptional activating properties in Saccharomyces cerevisiae.";
Submitted (JUN.1998) to the EMBL/GenBank/DDBJ databases.

BEBBL; AJ006637; CAAO7165.1;
NON_TER
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NCBI_TaxID=5659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmania major.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tortzakis N., Papageorgiou F.T., Tzinia A.K., Soteriadou K.P., "Identification and characterization of a novel Leishmania gene encoding for a putative histone H1- like transcription factor.", Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
      Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, mitosporic Saccharomycetales, Candida.
                                                                                                                                                                                                                                                                                                                                                                                      / Match 40.4%; Score 86; DB 3; Length 212; Local Similarity 48.9%; Pred. No. 0.31; hes 23; Conservative 10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Melo G.S., Fragoso S.P., Fasel N.S., Mendonca S.C.F., a "Cloning and sequencing of histone H1 gene from Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.9%; Score 85; DB 5; Length 98; llarity 55.0%; Pred. No. 0.19; Conservative 3; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (UL-2000) to the EMBL/GenBank/DDBJ databases EMBL, AP207632; AAG60608.1; -. InterPro; IPR001386; Histone_H1/H5. PR00624; HISTONEH5.
                                                                                                                                                                                                                                                                                                                               SEQUENCE 212 AA; 24231 MW; 10C2122E9554A387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 AA; 9999 MW; 0A4AB93089D6C261 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 АККРАККУАККРАККААККРАККРАККААККААККААКК
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leishmania amazonensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 kDa nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                            NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amazonensis.";
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BMY8
Q9BMY8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08W044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNP18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Q8WQ44
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BMY8
         SY RET REPRESENT SOC STATE OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Reissenbach J., Boucher C.A.,
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 86.5; DB 16; Length 200;
Pred. No. 0.27;
4; Mismatches 11; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                           Query Match 41.3%; Score 88; DB 16; Length 899; Best Local Similarity 58.7%; Pred. No. 0.82; Matches 27; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                     TIGREAMS; TIGRO1051; topA bact; 1.
PROSITE; PS00396; TOPOISOMERASE I PROK; 1.
DNA-binding; Isomerase; Topoisomerase; Complete proteome.
SEQUENCE 899 AA; 97723 MW; 1485DC4EDA0DA6FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                836 AKKPAKKAAATKSKAKAESDAPAKKTAA-KKPAAKKPAAKKAAPKA 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKAKAEKAK-KAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 AKKVAAKKVAAKKAPAKKAAVKKVAAKKAAPAKKAAVKKVAAKKA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 AA; 19279 MW; D3831B590510272D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AL646071; CAD16500.1; -.
InterPro; IPR00104; Antifreeze_1.
InterPro; IPR00393; treacle.
PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01503; TREACLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=GM11000;
MEDLINE=21681879; PubMed=11823852;
                                                               Topoisom; 1.
Pfam; PF01131; Topoisom bac; 1.
Pfam; PF01751; Toprim; 1.
Pfam; PF01396; zf-04 Topoisom; 1
PRINTS; PR00417; PRTPISMRASEI.
SMART; SM00437; TOP1AC; 1.
SMART; SM00436; TOP1BC; 1.
SMART; SM00436; TOPIBC; 1.
      Topoisom_bac; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probable histone H1 protein. RSC2793 OR RS00453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTA2. . Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 56.5
tes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
SEQUENCE 200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTA2p (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ralstonia.
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RESULT 8

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Best Loca Matches

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RESULT 9
093946
1D 09394
DT 01-N9
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DT 01-M
DE CTA2
OS CAA2

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Gaps

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101 AA; 10078 MW; 3D3AE865FD9B6846 CRC64;

SEQUENCE

Matches

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RESULT 12
10 08138
AC 08198
AC 08198
DT 01-JU
DT

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STRAIN=ESV-1; Dethe G., Pohl T., Knippers R., Mueller D.G., Boland W., Delaroque N., Bothe G., Pohl T., Knippers R., Mueller D.G., Boland W., "The complete nucleotide sequence of the Ectocarpus siliculosus virus
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ectocarpus siliculosus virus.
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Pred. No. 0.14;
4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, PR216291, AAR23175.1; -. EMBL, 189757, AAR66021.1; -. INTERPRO, IPR001386, Histone_H1/H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Jedrusik M.A., Schulze E.;
"The histone H1 complement of Caenorhabditis elegans.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The sequence of C. elegans cosmid C01B10.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D01ABB4CEC35566D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KKYAKKAKAEKAKKAY-KAAEAKKAAK-YEKAAAEKAAAKEAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 KKVAAKPKAPKVKKASPKKAAAPKAKKPVKKAAAKKSPAKKAA 56
                                                                                                                                     01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                           60 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 60 AA; 6212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.1%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BRISTOL N2;
Blanchard M., Bradshaw H.;
"The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00624; HISTONEHS
                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.; "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome.";
                                                                                                                                                                                                                                                                                  C01B10.5
                                                                        Q9U3W3
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   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                    2903W3
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                                                                                                        ACCOOR SERVING SERVING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
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EMBL, L37438; AAB59120.1; -. SEQUENCE 182 AA; 18252 MW; 9A17A397B12B0421 CRC64;
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NCBI_TaxID=5671;
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Bordetella.
   DB 5; Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.9%; Score 85; DB 5; Length 111; 55.0%; Pred. No. 0.21; tive 3; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 85; DB 2; Length 182;
Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H1-like nuclear protein.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF469106; AAL76335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 AA; 11162 MW; 16168F3B54960E83 CRC64;
                                                                                                                                                                             AKKYAKKAKAEK--AKKAY-KAAEAKKAAKYEKAAAEKAAKEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
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39.9%; Score 85; DB 5; 60.0%; Pred. No. 0.19; cive 2; Mismatches
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61.4%;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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                                                                    27; Conservative
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nes 22; Conservative
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01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 kDa nuclear protein.
Leishmania infantum.
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                                    Best Local Similarity
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Matches

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Best Local Similarity 52.3%; Pred. No. 1.2;
Matches 23; Conservative 5; Mismatches 15; Indels 1;
Submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF204951; AAK14566.1; -.
SEQUENCE 483 AA; 53368 MW; F85241B7B6A6913B CRC64;
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Search completed: March 10, 2003, 12:25:54 Job time : 25.8291 secs

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AAY82572 standard; peptide; 45 AA
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GenCore version 5.1.3
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Gapop 10.0 , Gapext 0.5
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213
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	Description	Copolymer molecula	Recombinant copoly	High affinity macr	Listeria monocytog						
SUMMAKIES	ID	AAY82572	AAY82577	AAY82573	AAY82575	AAY82576	AAY82574	AAY82571	AAR06446	AAR28871	ABB49123
	DB	21	21	21	21	21	21	21	11	13	23
	* Query Match Length DB I	45	109	56	77	86	99	35	106	46	239
	% Ouery Match	100.0	64.8	63.1	61.5	59.4	9.95	50.7	46.7	46.0	44.4
	Score	213	138	134.5	131	126.5	120.5	108	99.5	98	94.5
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(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

1154 11 AAR66445 223 20 AAY14928 224 21 AAY374055 234 22 ABG28693 33 19 AAW4934 198 19 AAW4936 205 21 AAR93082 205 21 AAR93097 205 22 AAG91997 207 22 AAG91997 208 22 AAG91997 209 22 AAG91997 2151 22 ABG60086 116 20 AAY14066 222 20 AAY14066 222 20 AAY14060 222 21 AAR91080 222 21 AAR91080 223 21 AAR91080 224 21 AAR91080 225 21 AAR91080 226 21 AAR91080 227 23 AAU1660 228 21 AAR91080 229 21 AAR91080 220 23 AAU1660759 220 23 AAU16609 221 AAR90180 221 AAR90180 221 AAR90180 222 21 AAR90180 223 21 AAR90180 223 21 AAR90180 224 AAR90180 225 21 AAR90180 226 21 AAR90180	Recombinant copoly		M. tuberculosis hi	•~	Mycobacterial hepa		Mycobacterial hepa	Mycobacterium bovi	C albicans apoptos	C glutamicum prote	Drosophila melanog	Drosophila melanog	Histone H1 isoform	Human histone H1.5	Histone H1 isoform	Human histone H1.5	Histone H1 isoform			Human histone H1 i	histone	Human histone H1 i	Human histone H1 i	Drosophila melanog	Human ORFX protein	Human ovarian anti	Human secreted pro	Human secreted pro	Human ribosomal L1	Human secreted pro	Lung cancer associ	Streptococcus pneu	Polycationic polyp	Protamine-like pep
# W # # # # W W W W C 10 W - W W W W W W W W W W W W W W W W W					-		AAW4493	AAB2057		AAG9199	ABB6327	ABB6008	•					·	AAW2947					•	-	•	AAG0075	AAG0075		AAG0075	-	_	•	
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## ALIGNMENTS

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromlmetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; (crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2. 98US-0101693. 99WO-US22402 WO200018794-A1 25-SEP-1998; 24-SEP-1999; Unidentified 06-APR-2000. 

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for all the invention are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for the diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases in conditions, e.g. multiple contitions, autoimmune oophoritis, autoimmune thyroiditis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune oophoritis, autoimmune thyroiditis, autoimmune cophoritis, autoimmune thyroiditis, autoimmune cophoritis, autoimmune thyroiditis, autoimmune vecetunitis, crohn's disease, diabetes mellitus, Graves disease, dullain-Barre's syndrome, Hashimoto's disease, mallitus, Crohn's disease, diabetes mellitus, crohn's disease, diabetes mellitus, crohned host-versus-graft disease, giraft-versus-seried disease, and delayed-type hypersenaitivity. The polypeptides of the invention have defined molecular weights and physecial properties which are analogous to molecular weights and physecial properties which are analogous to molecular mellicaner acetate molecules, which makes them ideal for use as
                                                                                                                                            Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                  Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   molecular weight markers.
                                                                                  WPI; 2000-317499/27.
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45 AA; Seguence

Gaps .; 0 100.0%; Score 213; DB 21; Length 45; 100.0%; Pred. No. 1.4e-16; ive 0; Mismatches 0; Indels Local Similarity 100. ses 45; Conservative Query Match Matches

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AAY82577 standard; peptide; 109 AA

AAY82577;

(first entry) 28-JUL-2000 Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; hemostatic; antiporiatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn; disease; chronic immune thromboortopeania purpura; colitis; diabetes mellitus; Graves disease; duillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. 

WO200018794-A1.

06-APR-2000

99WO-US22402. 24-SEP-1999;

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight cand an amino acid composition corresponding to the copolymer. The cand an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer accetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune continued architect and include aither cell-mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple antibody-mediated diseases and inflammatory conditions, e.g. multiple condering diseases and inflammatory conditions, e.g. multiple acceptantis, autoimmune based, succimmune haemolytic ansemia, autoimmune ophoritis, autoimmune thrombocytopaenia cueoretinitis, contact sensitivity disease, diabetes mellitus, Graves purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves Calsease, Guillann-Barre's syndrome, Hashimoto's diseases, and myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic include host-versus-graft disease, graft-versus-praft disease, graft-versus-bost disease, and delined molecular weights and physical properties which are analogous to glatized and properties which makes them ideal for use as
                                                                                                                                                                                                                                      Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.8%; Score 138; DB 21; Length 109; 76.6%; Pred. No. 5.1e-08; .ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                             Claim 10; Page 14; 72pp; English.
                                                                (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                      98US-0101693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 76.6
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molecular weight markers.
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                                                                                                                                          Lis D;
                      25-SEP-1998;
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                                                                                                                                          Gad A,
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Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3. 65 AKKYAKAAKAE--KKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109 AAY82573 standard; peptide; 56 AA. 28-JUL-2000 (first entry) AAY82573; RESULT 3 AAY82573 g 

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glatiramer acctate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyrominetic; haemostatic; antibaoriatic; dermatory; antidabetic; thyrominetic; haemostatic; antipaoriatic; dermatorological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guilain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer; molecular weight marker; TV-marker; immune disease;

Unidentified

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                           MAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer accetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include archritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune thoromocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves burpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, myasthenia gravis, psoriabilis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and phylpeptides of the invention have defined molecular weights and phylpeptides of the invention have defined molecular weights which makes them ideal for use as
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                                                                                                                                                                                                                                                                                                   Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 14; 72pp; English
                                                                                                                                                          (YEDA ) YEDA RES & DEV CO LTD (TEVA-) TEVA PHARM USA INC.
                                                                                                                    98US-0101693.
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Best Local Similarity 68.4%;
Matches 39; Conservative
                                                                               99WO-US22402
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WO200018794-A1
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                                                                                                                    25-SEP-1998;
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MAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular meight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic uveoretinits, crohn's disease, chronic immune thyroidutis, autoimmune unamental autoimmune cophoritis, autoimmune thyroiditis, autoimmune cure uveoretinitis, crohn's disease, chronic immune thrombocytopaenia purque, collitis, conteat sensitivity disease, diabetes mellitus, Graves disease, duillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, peoriasis, pemphigus vulgaris, or systemic luna, a prace and a present and a prace and a prace and a present and a prace and
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Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
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Pred. No. 2e-07;
0; Mismatches 6; Indels 3
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                                                 pemphigus vulgaris; systemic lupus erythematosus
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ilarity 50.6%;
Conservative
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es 39; Conserv
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                                                                                                                                                          Unidentified.
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RESULT 6

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antibody-mediated diseases. Such diseases include archritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune opportitis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, dilabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have
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                                        glatitamer acctate, autoimum disease, antiatthritic, neuroprotective, osteopathic, immunosuppressive, antithyroid, antiinflammatory, antiantediabetic: thyromimetic; harmostatic; dermaclogical, antiansemic; immunosuppressive, demyelinating disease, osteoarthritis; inflammatory condition, multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura, colitis; diabetes mellitus; Graves disease; duillain-Barre's syndrome; psoriasis; pemphigus vulgaris; systemic lupus erythematosus.
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                         Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuropr
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(TEVA-) TEVA PHARM USA INC.
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                                                                                                                                                                                                                                                                                        Unidentified
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                                                            41;
                             59.4%; Score 126.5; DB 21; Length 86; 45.3%; Pred. No. 7.1e-07;
                                                            6; Indels
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                                                            0; Mismatches
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                                                          39; Conservative
                                          Local Similarity
86 AA;
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight cand an amino acid composition corresponding to the copolymer. The colypeptides of the invention are used as molecular weight markers for polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing include either cell-mediated or diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, cantibody-mediated diseases. Such diseases include arthritic conditions, cantemia, autoimmune ophoritis, osteoarthritis, autoimmune haemolytic ansemia, autoimmune ophoritis, autoimmune thrombocytopaenia cuecertinitis, contact sensitivity disease, diabetes mellitus, Graves Co disease, Guillain-Barres syndrome, Hashimoto's disease, midipathic myxocdema, myasthenia gravis, psoriated disease, which can be treated condingue erythematosus. Mediated-mediated diseases which can be treated condingue erythematosus weights and physical properties of the invention have condingue mysochema majogus to delined molecular weights and physical properties which mare analogous to delined molecular weights and physical properties which mare analogous to malon.
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                                                                                                                                                                                                          glatitamer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antichyroid; antinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guilain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
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                                                                                                                                                   Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.
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                                                                                                                                                                                           Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                      AAY82574 standard; peptide; 66 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0101693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US22402.
                                                                                                      (first entry)
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Best Local Similarity 71.1
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200018794-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-1998;
                                                                                                        28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2000.
                                                              AAY82574;
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AAY8257
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2,

Gaps

10;

Indels

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Length 35;

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1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA
                            AAY82571 standard; peptide; 35 AA.
                                                                                                                                                                                                 Claim 10; Page 14; 72pp; English.
                                                                                                                                      99WO-US22402.
                                                                                                                                               98US-0101693
                                            28-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                       nolecular weight markers
                                                                                                                                                                            WPI; 2000-317499/27.
                                                                                                                                                      (YEDA ) YEDA RES & (TEVA-) TEVA PHARM
                                                                                                                                                                                                                                                                                                               35 AA
                                                                                                                     WO200018794-A1.
                                                                                                                                                                    Gad A, Lis D;
                                                                                                                                               25-SEP-1998;
                                                                                                                                      24-SEP-1999;
                                                                                                            Jnidentified
                                                                                                                             06-APR-2000.
                                     AAY82571;
                                                                                                                                                                                                                                                                                                               Sequence
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segments: YKK, AAB, KAK, EKA, KKA, YEA, AKA KEA, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control ademyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing genes encoding random polymers of aminoacid(s) - 1 producing recombinant polypeptide(s) with biological and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant copolymer 1-19, myelin basic protein analogue.
                                                                                                                                                                   1 AKKYAKKEKA--AKKAYK-----KEAKAKAAEAAKEAAYEA 35
                                                                                                                  1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA
Score 108; DB 21;
Pred. No. 2.9e-05;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                       AAR06446 standard; protein; 106 AA
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     50.7%;
ilarity 64.4%;
Conservative
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89US-0312541.
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     Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ06446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-FEB-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                      03-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                 Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidabetic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; ornonic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; pemphigus vulgaris; systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                   Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.
                            99
                      29 AKKYAKAAKAE--KKEYAAAEAK-----YKAEAAKAAAKEAAYEA
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5

Gaps

6

Indels

Score 99.5; DB 11; Pred. No. 0.00076; 4; Mismatches 7;

Query Match
Best Local Similarity 58.3%;
Matches 28; Conservative

Length 106;

the following

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92WO-US03609.
                                                                                                                   91US-0694983.
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                                                                                                                                    (UNIW ) UNIV WASHINGTON
                         /note=
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                                                                                                                                                                        WPI; 1992-398516/48.
                 46
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                                                                                                                                                                                                                                                                                                                                                                                                                        46 AA;
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                Modified-site
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                                                                                                 01-MAY-1992;
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                                                             WO9219248-A
                                                                               12-NOV-1992
                                                                                                                                                     Stahl PD;
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Best Local
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                                                                                                                                              mannose receptor;
                                                                                                                                           glycopeptide; mannose; mannosylated; glycosylated; mannose receptor; macrophages; monocytes; destroy; cytotoxicity; label; inage; alter; macrophage processing of antigen, MRC restriction; inflammation; inflammatory disease; macrophage secretory products; Crohn's disease; legionnaires disease; mononuclear phagocytes; HIV; AIDS; lysosomal storage disease; Gaucher's disease; asthma; alveolar macrophages metastasis; systemic macrophages; deliver; antigenic peptides; prevent transplant rejection; organ transplantation; antitumour agents; cancer; toxins.
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                                                                                                                                                                                                                                                                                                                                                                                                                        fucose, glucose
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                                                                                                                          High affinity macrophage mannose receptor ligand compound #9.
                                                                                                                                                                                                                                                                                   N-Ac-glucosamine. May also have non interfering substits."
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                  8 KAAKKAYEAEKAKAEKKAEKAEKAEKAABEKKAKEAKKAEKAEKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "opt may have mannose, fucose,
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       KYAKKA-KAEKAKKAYKAAEAKKAAKYEKAAAEKAA-
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                                                                     AAR28871 standard; peptide; 46 AA
                                                                                                         (first entry)
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/note=
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                                                                                                         23-MAR-1993
                                                                                                                                                                                                                                      Synthetic.
                                                                                       AAR28871;
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                                                            AAR2887
                                                    RESULT
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This compound represents a glycopeptide effective in inhibiting the binding of labelled mannosylated BSA to mannose receptors. Mannose receptors are uniqualy found on macrophages and not on manocytes. Glycopeptides such as this provide a mechanism to target macrophages captions the provide a mechanism to target macrophages appecifically, to image, label, destroy or otherwise alter their antigen processing function. In addition they can be conjugated to antigen processing function. In addition they can be conjugated to altigen processing function. In addition they can be conjugated to cold supports and used to purify mannose receptors from a variety of sources. They are useful in the treatment of inflammatory diseases driven by macrophages ecretory products eg. Crohn's diseases infectious diseases in which macrophages harbour replicating infectious agents eg. Legionnaires disease, viral infections involving mononuclear phagocytes eg. HIV and lysosomal storage diseases, in which macrophages are principally involved eg. Gaucher's disease, asthma mediated by systemic macrophages. The peptides controlling metastasis, mediated by systemic macrophages to a macrophage to marshal an immune response; also self peptides to prevent tissue transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
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                                                                                                                                    or
/note= "opt may have mannose, fucose, glucose or
N-Ac-glucosamine."
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                                                                                                                                    glucose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New high affinity mannose receptor ligand cpds. - for tidiseases mediated by macrophage activity e.g. asthma, inflammatory diseases and infectious diseases, e.g. HIV
                                                                                                                           "opt may have mannose, fucose, g
N-Ac-glucosamine. May also have
interfering substits."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.0%; Score 98; DB 13;
63.4%; Pred. No. 0.00047;
ive 1; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listeria monocytogenes protein #1827.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 21; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB49123 standard; Protein; 239
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coding for TCOP-1-77 were subcloned from PREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and TCOP-1 sequences. A methionine residue occurs between the Protein A and TCOP-1 sequences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. TCOP-1-77 contains oligonuclectide duplexes incoding the following segments: YKK, EAE, KAK, AAK, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The product prevents or arrests experimental autoimmuse encephalomyelitis. They are used to prevent, arrest or control sdemyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                        improve the expression of rCOP-1 polypeptides in E. coli,
                                                                                                                                                                                                                                                                                                                       Producing genes encoding random polymers of aminoacid(s) - 1 producing recombinant polypeptide(s) with biological and/or
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 11; 25pp; English
                                                                                                       90US-0473845.
89US-0312541.
                                                             90EP-0301700.
                                                                                                                                                                                                                                                                                                                                                                     immunological activity
                                                                                                                                                                       (REPL-) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             certain amino acids.
                                                                                                                                                                                                                                                          WPI; 1990-255848/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See also AAQ05665
                                                                                                                                                                                                                                                                               N-PSDB; AAQ05664
                                                             16-FEB-1990;
                                                                                                       07-FEB-1990;
17-FEB-1989;
                    22-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                  Cook KS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
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à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and continuous and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome caquence and proteins selecting compositions for the treatment or prevention of infections by L. Monocytogenes and related organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                  Cossart P;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                                                                                                                                                                                           Dehoux P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                             ani F, Nedjari H, Glaser P, Kunst F, Cossart,
Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
Garrido-Garcia P, Tierrez-Martinez A, Amend A
nn E, Hain T, Berche P, Charbit A, Durant L;
ro F, Garcia Del Portillo F, Gomez-Lopez N;
os B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                               Durant L;
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                                                                                                                                                                                         Feihi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; SEQ ID No 1828; 192pp; French.
                                                                                                                                                                                           Couve E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR06445 standard; protein; 154 AA
                                                                                                                                                                                                               Dubsuz,
Daniels J, Goeber,
Daniels J, Goeber,
Dominguez-Bernal G, Garrido-
Chakraborty T, Domann E, H
Perez-Diaz J, Baquero F, C

Maduenio E, De Pablos B, I
                                                             11-APR-2001; 2001WO-FR01118.
                                                                                                     11-APR-2000; 2000FR-0004629
                                                                                                                                                                                         Buchrieser C, Frangeul L,
Dussurget O, Chetouani F,
Daniels J, Goebel W, Kref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 56.2%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             related polypeptides
                                                                                                                                              (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-010914/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 AA;
                  18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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AC AAR0
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KX
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KW RECX
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KW IMM
KW MU11
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PN EP3:
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                                 Gaps
                                 ;
9
44.1%; Score 94; DB 11; Length 154; 60.5%; Pred. No. 0.0044; ive 2; Mismatches 9; Indels
                                                                                    105 KKYKKKAKKAKKAKYKK--KAKEAEKA----KAAAEAEKAKEAEYK 141
                                                                2 KKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYE 44
     0.0044;
                                                                                                                                                                                                                                                                                Amino acid sequence of M. vaccae antigen GV-45.
                                                                                                                                                                                 Ą.
                                                                                                                                                                               AAY14928 standard; protein; 223
                                                                                                                                                                                                                                               25-OCT-1999 (first entry)
                Local Similarity 60.5
tes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium vaccae
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9932634-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1999
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Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; mmunological activity; autoimmune encephalomyelitis;

multiple sclerosis;

EP383620-A Synthetic

Recombinant

Recombinant copolymer 1-77, myelin basic protein analogue.

(first entry)

03-JAN-1991

AAR06445;

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The invention provides a method for the diagnosis, prevention and treatment of ulcerative colitis (UC) using histone H1-like antigen, a porini antigen or a Bacteroides antigen as a target antigen. The novel method of diagnosing UC in a subject suspected of having inflammatory bowel disease (IBD) comprises: (1) obtaining a sample from the subject; (2) contacting the sample with a histone H1-like antigen, or perinuclear anti-neutrophil cytoplasmic antigen, or the pANCA-reactive fragment, complex of the histone H1-like antigen, and (3) detecting the presence or absence of the complex; and antibody to the histone H1-like antigen; and (3) detecting the presence or absence of the complex; indicates that the subject has UC. The pANCA-reactive histone H1-like antigen are useful in the antigen, porin antigen and Bacteroides antigen are useful in the diagnosis, prevention and treatment of UC. The methods can also be used for identifying agents useful for treating UC. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing ulcerative colitis or susceptibility, by detecting complex formation between microbial porin antigen and perinuclear anti-neutrophil cytoplasmic autoantibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ulcerative colitis; inflammatory bowel disease; porin antigen; MAD;
pANCA; perinuclear anti-neutrophil cytoplasmic antibody; 214 protein;
histone H1; isoform.
                                                                                                                                      Use of histone H1, porin or Bacteroides antigens as targets for the diagnosis, prevention and treatment of ulcerative colitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.0%; Score 89.5; DB 20; Length 214; 55.6%; Pred. No. 0.019; 11ve 4; Mismatches 13; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M. tuberculosis histone H1-like protein, 214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY57353 standard; Protein; 214 AA
                                                                                                                                                                                                             Claim 2; Fig 11; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0041889.
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97US-0837058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Conservative
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA.
                                                                                        WPI; 1999-551215/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                              Cohavy 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cohavy O, Braun J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                              Braun J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY57353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. vaccae proteins. The M. vaccae proteins may be employed to activate T cells and natural killer cells, to stimulate the production of cytokines, to enhance the expression of cy-stimulatory molecules on dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The proteins can be expressed by standard recombinant methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins or nucleic acid sequences encoding the proteins or nucleic acid sequences encoding the proteins in the compounds and diseases, immune disorders and cancer. In particular, the compounds and methods are used for treatment of diseases of the respiratory system, such as mycobacterial infections, asthma, allergies, tuberculosis, leprosy, sarcoidosis and lung cancers, and disorders of the skin such as posciasis, atopic dermatitis, eczema, allergic contact dermatitis, alopecia areata, and skin cancers such as basal carcinoma, squamous cell carcinoma and melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ulcerative colitis; histone; H1-like antigen; porin antigen;
Bacteroides antigen; inflammatory bowel disease; IBD; pANCA; diagnosis;
perinuclear anti-neutrophil cytoplasmic antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides heat-killed Mycobacterium vaccae, or recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
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42.7%; Score 91; DB 20; Length 223;
Best Local Similarity 59.6%; Pred. No. 0.014;
Matches 28; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                               Prestidge RL, Skinner MA, Tan P, Visser ES, Watson J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 AKKAATKAAPAKKATAAKKAAPAKKATAAKKAAPAKKAATKA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYA-KKAKAEKAKKAYKAAEAKKAAKYEKAA-AEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M. tuberculosis histone H1-like antigen.
                                                                                                                                                                                                                                                                                                                                                                                                  Enhancing immune response to an antigen
                                                                                                                                                                                                                                 (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY34055 standard; protein; 214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 239; 243pp; English.
                                                                                     97US-0996624.
97US-0997080.
97US-0997362.
                      98WO-NZ00189
                                                                  98US-0205426
                                                                                                                                                            98US-0095855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                              WPI; 1999-430163/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 AA;
                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ11393
                      23-DEC-1998;
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                                                                  04-DEC-1998;
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23-DEC-1997
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                                                                                                                                                                      designated 214.
                                     The invention provides a method for diagnosing ulcerative colitis in a
                                                     subject suspected of having inflammatory bowel disease. The method comprises reacting a patient sample with a porin antigen that is immunologically reactive with pANCA (perinuclear anti-neutrophil cytoplasmic antibodies) and detecting formation of a Ag-pANCA complex as indicative of ulcerative colitis. The method is used to diagnose ulcerative colitis to it. The present sequence represents a histone HI-like protein of M. tuberculosis, designated 21
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                       Э,
                                                                                                                                                                                                                                                Score 89.5; DB 21; Length 214;
Pred. No. 0.019;
4; Mismatches 13; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                 111 AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
                                                                                                                                                                                                                                                                                                                           1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 59052; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #28684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG28693 standard; Protein; 334 AA
Example 5; Fig 10; 49pp; English
                                                                                                                                                                                                                                              42.0%;
55.6%;
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                   Local Similarity 55.6 tes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-639362/73.
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                                                                                                                                                                                                              214 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS92880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-2002
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                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG28693;
                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1:
ABG28693
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diagnostics, forensics, gene mapping, identification of mutations

C responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC antino acid sequences. ABG00010-ABG30377 represent novel human

CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this parent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ sequence 334 AA;

Query Match

40.8%; Score 87; DB 22; Length 334;

Best Local Similarity 57.4%; Prec. No. 0.056;

Matches 27; Conservative 6; Mismatches 12; Indels 2; Gaps 2;
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Search completed: March 10, 2003, 12:21:28 Job time : 24.4494 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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March 10, 2003, 12:26:10 ; Search time 13.3861 Seconds
 (without alignments)
141.764 Million cell updates/sec protein search, using sw model OM protein Run on:

US-09-816-989A-2 Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 Scoring table:

**BLOSUM62** 

188354 Total number of hits satisfying chosen parameters: 188354 segs, 42170167 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| cgri2\_6/ptodate/1/pubpaa/USO8\_NEW\_PUB.pep:\*
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| cgri2\_6/ptodatea/1/pubpaa/USO7\_PUBCOMB.pep:\*
| cgri2\_6/ptodatea/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
| cgri2\_6/ptodatea/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
| cgri2\_6/ptodatea/1/pubpaa/USO8\_PUBCOMB.pep:\* 6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\* 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:\* 6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\* 6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\* /ggn2\_6/prodata///pubpaa/USO9\_PUBCOMB.pep:\* /cgn2\_6/prodata///pubpaa/USI0\_NEW PUB.pep:\* /cgn2\_6/prodata///pubpaa/USI0\_PUBCOMB.pep:\* /cgn2\_6/prodata///pubpaa/US60\_NEW PUB.pep:\* /cgn2\_6/prodata///pubpaa/US60\_PUBCOMB.pep:\* Published\_Applications\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	1-2 Sequence 2, Appli	Sequence 7,	Sequence 3,	Sequence 5,	Sequence 6,	Sequence 4,	Sequence 1,	Sequence 201,	Sequence 5751	24 Sequence 24, Appl	Sequence 2,		S	.27 Sequence 27, Appl				3187	
Ü	US-09-816-989A-2	US-09-816-989A-	US-09-816-989A-3	US-09-816-989A-5	US-09-816-989A-6	US-09-816-989A-4	US-09-816-989A-1	US-10-051-643-201	US-09-738-626-5751	US-09-820-843A-24	US-09-923-304-2	US-09-925-302-559	US-09-820-843A-23	US-09-820-843A-27	US-09-820-843A-8	US-09-882-774-1	US-09-765-272-160		
DB	107	10	10	10	10	10	10	σ	σ	σ	10	10	0	σ	0	σ	10	10	10
Query Match Length DB	45	109	26	77	98	99	35	223	165	309	220	265	352	356	372	619	641	1156	241
Query Match	100.0	64.8	63.1	61.5	59.4	56.6	50.7	42.7	38.5	36.6	35.4	35.4	34.7	34.7	34.0	33.1	32.9	32.9	31.9
Score	213	138	134.5	131	126.5	120.5	108	91	82	78	75.5	75.5	74	74	72.5	70.5	70	70	68
Result No.	-	7	m	4	ß	ø	7	80	O	10	11	12	13	14	15	16	17	18	19

Sequence 127, App Sequence 5, Appli Sequence 10314, A Sequence 10314, A Sequence 7, Appli Sequence 13, Appli Sequence 13, Appli Sequence 95, Appli Sequence 90, Appli Sequence 90, Appli Sequence 90, Appli Sequence 100, Appli Sequence 17061, Appli Sequence 17, Appli Sequence 17, Appli Sequence 117, Appli Sequence 10575, A Sequence 10575, A Sequence 10575, A Sequence 1057, Appli Sequence 1057, Appli Sequence 1057, Appli Sequence 1057, Appli Sequence 11554, Appli Sequence 11564, Appli Sequence 11516, Appli Sequence 11554, Appli Appl	
10 US-09-771-161A-127 9 US-10-184-832-5 10 US-09-815-242-10314 9 US-09-815-242-13765 9 US-09-815-242-13765 9 US-09-815-242-13765 9 US-09-815-242-13765 10 US-09-919-497-100 9 US-09-919-497-100 9 US-09-919-48 10 US-09-99-724-48 10 US-09-99-724-48 10 US-09-99-724-48 10 US-09-99-724-46 10 US-09-99-724-46 10 US-09-915-233-11 10 US-09-915-242-10575 10 US-09-915-242-10575 10 US-09-815-242-10575 10 US-09-815-242-10575 10 US-09-815-242-10575 10 US-09-815-242-10575 10 US-09-815-242-10575 10 US-09-815-242-10575 10 US-09-815-242-10575 10 US-09-815-242-10575 10 US-09-815-242-10516 10 US-09-815-242-11216 10 US-09-815-242-11216	
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# ALIGNMENTS

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APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
TITLE OF INVENTION: ADD FOR THERAPEUTIC USE
TITLE OF INVENTION: ADD FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
RRIOR APPLICATION NUMBER: PCT/US99/22402
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
Sequence 2, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
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Length 45; 1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45 1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45 100.0%; Score 213; DB 10; ilarity 100.0%; Pred. No. 2.2e-16; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 45; Conserv US-09-816-989A-7 유 ઠ

; Sequence 7, Application US/09816989A ; Patent No. US20020115103A1 ; GENERAL INFORMATION: ; APPLICANT: Gad, Alexander ; APPLICANT: Lis, Doris

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Gaps

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CURRENT APPLICATION NUMBER: US/09/816,989A
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Matches
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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REPERENCE: 2609/60807-A-P-CT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT PELLING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR FILING DATE: 1998-09-25 PRIOR FILING DATE: 1998-09-24 NUMBER: OF SEQ ID NOS: 7 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Dorise
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION UNMERR: US/09/816, 989A
CURRENT FILLING DATE: 12004-03-25
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1996-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PARENTIN VERSION 3.1
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Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 64.8%; Score 138; DB 10;
Best Local Similarity 76.6%; Pred. No. 3.6e-08;
Matches 36; Conservative 0; Mismatches 7;
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Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 68.4%;
Matches 39; Conservative
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ORGANISM: Artificial Sequence
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LENGTH: 56
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APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
TITLE Gad, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR 105/09/816,989A
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 1999-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
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                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 77;
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Best Local Similarity 45.3%; Pred. No. 4.5e-07;
Matches 39; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.5%; Score 131; DB 10;
llarity 50.6%; Pred. No. 1.4e-07;
Conservative 0; Mismatches 6;
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CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
LENGTH: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 -KAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YKAEAAKAAKEAAYEA 77
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hes 39; Conserva
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       of Immunologically-Mediated Diseases of the Respiratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       42.7%; Score 91; DB 9; Length 223
59.6%; Pred. No. 0.0059;
tive 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 AKKAATKAAPAKKATAAKKAAPAKKATAAKKAAPAKKAAPAKKAATKA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
TITLE OF INVENTION: of Immunologically-Mediated Diseases
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REFERENCE: 11000.10082
CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 2002-01-18
FRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 201
LENGTH: 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 82; DB 9;
Pred. No. 0.038;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
LENGTH: 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: OZAKI, AKIO
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5751, Application US/09738626
Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/09820843A; Publication No. US20030039963A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mycobacterium vaccae US-10-051-643-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 38.5%;
Best Local Similarity 62.9%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 59.69
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 249-125
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US-09-820-843A-24
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                     APPLICANT: Lis, Doris

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERADEUTIC USE
CURRENT APPLICATION NUMBER: US/09/816,989A
PRIOR APPLICATION NUMBER: 2001-03-23
PRIOR APPLICATION NUMBER: POT/010,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT PILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
NUMBER OF SEQ ID NOS: 7
SOPTWARE: Patentin Version 3.1
SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.6%; Score 120.5; DB 10; Length 66; ilarity 71.1%; Pred. No. 1.4e-06; Conservative 0; Mismatches 6; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.7%; Score 108; DB 10; Length 35; 64.4%; Pred. No. 1.5e-05; Live 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 201, Application US/10051643
Publication No. US20020197265A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
ITILE OF INVENTION: Methods and Compounds for the Treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 AKKYAKAAKAE--KKEYAAEAK-----YKAEAAKAAKEAAYEA 66
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Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 29; Conserva
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les 32; Conserv
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                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
LENGTH: 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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7;

Indels

Length 265;

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APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REPERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Petentin version 3.0
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/09820843A

Sequence 27, Application US_030039963A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Council Of Scientific and Industrial Research
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A

CURRENT FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 118

SOFTWARE: Petentin version 3.0

SEQ ID NO 27
                                                                            FEATURE:
NAME/KEY: SITE
LOCATION: (4)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-559
                                                                                                                                                                                                                                                                                                                                                                            213 AKKITAASKKAPAQKVPAQKATGQKAAAPAPKAQKGQKAPAQKAPAPKAS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.7%; Score 74; DB 9; Length 352; 51.1%; Pred. No. 0.56; tive 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                 160 AKPAAKPAAKPAAKTAAAKPAAKPTAKPAAKPAAKPAAKTA 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc feature
NAME/KEY: misc feature
NAME/KEY: misc feature
NAME/KEY: misc feature
OTHER INFORMATION: gi|9951563
                                                                                                                                                                                                                                       Query Match 35.4%; Score 75.5; DB 10; Best Local Similarity 51.0%; Pred. No. 0.29; Matches 25; Conservative 7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-820-843A-23
; Sequence 23, Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: colA protein
NAME/KEY: misc_feature
OTHER INFORMATION: gi|9656364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 51.1
Matches 23; Conservative
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ORGANISM: Vibrio cholerae
                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-09-820-843A-27
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        LENGTH: 265
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APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION WITHMER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
SEQ ID NO 24
LENGTH: 309
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Patent No. US20020081612A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KITH
APPLICANT: VIANG, FENG
TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
TILE REPRENCE: UTSC:658US
CURRENT APPLICATION NUMBER: US/09/923,304
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 11
SCOTWARR: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 220
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                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature;
CTHER INFORMATION: polyhydroxyalkanoate synthesis protein PhaF;
NAME/KEY: misc_feature
;
OTHER INFORMATION: gi|9951352
US-09-820-843A-24
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Pred. No. 0.24;
7; Mismatches 10; Indels 7
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CHARLE REFERENCE:
FILE REFERENCE: PALO4
CURRENT APPLICATION NUCLEIC ACIDS, Proteins and Antibodies
FILE REFERENCE: PALO4
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/US00/05918
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PALENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 78; DB 9; Length 309;
Pred. No. 0.19;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 AKKITAASKKAPAQKVPAQKATGQKAAPAKAQKGQKAPAQKADARKAS 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 559, Application US/09925302; Patent No. US20020044941A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.8%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.4%;
Best Local Similarity 51.0%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-304-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-925-302-559
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                                                                                                                                                                                                                                                                    TYPE: PRT
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Sequence 8, Application US/09820843A

Sequence 8, Application US/09820843A

Publication No. US20030039963A1

GENERAL INFORMATION:
APPLICANT:
COUNCIL OF Scientific and Industrial Research
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A

CURRENT PILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0

SEQ ID NO 8
LENGTH: 372
TYPE: PRT
CURRENT: PRINCE OF SEQ ID NOS: 108
SOFTWARE: PRT
CORRENT: 172
CORRENT: 173
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34.0%; Score 72.5; DB 9; Length 372;
Best Local Similarity 44.7%; Pred. No. 0.85;
Matches 21; Conservative 8; Mismatches 15; Indels
                                                                                                       Query Match 34.7%; Score 74; DB 9; Length 356; Best Local Similarity 45.5%; Pred. No. 0.57; Matches 20; Conservative 4; Mismatches 20; Indels
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CTHER INFORMATION: outer membrane integrity protein (tolA)
NAME/KEY: misc feature
CTHER INFORMATION: gi|1573353
US-09-820-843A-8
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US-09-820-843A-27
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US-09-820-843A-8
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Search completed: March 10, 2003, 12:53:42 Job time: 13:5289 secs

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INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 223 amino acids STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 98121
39, Appl
40, Appl
3, Appli
3, Appli
13, Appli
15, Appli
15, Appli
16, Appli
11, Appli
12, Appli
13, Appli
14, Appli
26, Appli
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26, Appli
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                                                                                                                                  March 10, 2003, 12:15:04 ; Search time 7.97468 Seconds
    (without alignments)
166.029 Million cell updates/sec
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Sequence 3
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1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*

6: /cgn2_6/ptodata/2/laa/pcTUS_COMB.pep:*
                  GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-150-812-26
                                                                                                                                                                                                                                                                                                                                                               262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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213
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                                                                                                                                        Run on:
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No.
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Sequence 39, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC PANCA antigens
                                                                                                                                                                                                                                                                                                                                                                                                                            42.0%; Score 89.5; DB 3; Length 214; 55.6%; Pred. No. 0.0067; tive 4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db . 111 AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 92122
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CAMPBERSEE: CAMPBELL & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 535-9901
TELEPAX: (619) 535-9001
                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: CAMDDELI, CALINTYN A.
REGISTRATION NUMBER: 31,815
REFERRINCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 103 amino acids
amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.64
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-041-889-27
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; MOLECULE TYPE:
US-09-041-889-39
  FILING DATE
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STATE: Ca
COUNTRY:
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Fatent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                    7
                                                                                    Gaps
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                                                                                                                                                                                                                                                              Length 223;
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                                                                                 12; Indels
                                                                                                                                               137 AKKAATKAAPAKKATAAKKAAPAKKATAAKKAAPAKKAAPAKKAATKA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYA-KKAKAEKAKKAYKAAEAKKAAKYEKAA-AEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                     42.7%; Score 91; DB 4;
59.6%; Pred. No. 0.0048;
tive 5; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Mycobacterium vaccae US-09-205-426-201
                                     Query Match
Best Local Similarity 59.6
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
US-09-095-855-201
                                                                                                                                                                                                                               RESULT 2
US-09-205-426-201
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LENGTH: 223
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Gaps

3,

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6033864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 158 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-09-041-889-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                          COUNTRY:
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Ulcerative Colitis, and Clinical Subtypes Thereof, Using
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                                       Gaps
                                       8;
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 36.2%; Score 77; DB 3; Length 103;
52.2%; Pred. No. 0.068;
iive 1; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.2%; Score 77; DB 3; Length 116; 52.2%; Pred. No. 0.077; tive 1; Mismatches 13; Indels
                                                                      51 AKPKAKKAGAAKAKKPAGATPKKAKKAAGAKKAVKKTPKKAKKPAA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASIPICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Carthryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-PM 3006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-09-041-889-40
is Sequence 40, Application US/09041889
is Patent No. 6033864
is GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
ittle OF INVENTION: Diagnosis, Prev
ITTLE OF INVENTION: Ulcerative Coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 52.2'
Matches 24; Conservative
Query Match
Best Local Similarity 52.2
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide US-09-041-889-38
                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Diagnosis, Prevention and Treatment of
Ulcerative Colitis, and Clinical Subtypes Thereof, Using
Microbial UC pANCA antigens
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                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FOLDS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/041,889

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION:

PRIOR APPLICATION:

PRIOR APPLICATION:

APPLICATION NUMBER: US 08/837,058

FILING DATE:

APPLICATION NUMBER: 31,815

FERENCE/DOCKET NUMBER: 31,815

REGISTRATION FOR SEQ ID NO: TELEFPHONE: (619) 535-9801

TELEFPHONE: (619) 535-9801

INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS:

LEMETHE THE THE TABLE TO THE TABL
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APPLICANT: Braun, Jonathan
APPLICANT: Braun, Jonathan
APPLICANT: Chavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatn
TITLE OF INVENTION: Ulcerative Colitis, and Clinical
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
TITLE OF INVENTION: Microbial UC pANCA antigens NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 77; DB 3;
Pred. No. 0.11;
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36.2%; Score 77; DB
Best Local Similarity 52.2%; Pred. No. 0.11
Matches 24; Conservative 1; Mismatches
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Query Match
Best Local Similarity
Matches 24; Conserv
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US-09-041-889-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKAKAEKA-----KKAYKAAEAKKAAKYEKAAEKAAA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CUBRENT PELICATION DATA:
FILING DATE:
FLING DATE:
FLING DATE:
FLING PATE:
FLING DATE:
FLING PATE:
FLING PATE:
FLING PATE:
FLING PATE:
FLING PATE:
FREERENCE/DOCKET NUMBER: 9-PM 2438
TELECOMMUNICATION INFORMATION:
FREERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
RELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-901
TELEPHONE: (619) 535-904
SOFTWARE CHARACTERISTICS:
LENGTH: 222 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: mino acide
                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1.222
OTHER INFORMATION: /note= "product = Human Histone
OTHER INFORMATION: H1-S-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                    FILING DATE: 11.APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Carthryn A.
REGISTRATION NUMBER: 31.815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
APPLICATION NUMBER: US 08/837,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-837-058-3
; Sequence 3, Application US/08837058
; Patent No. 6074835
; RENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Targan, Stephan R.; TITLE OF INVENTION: Diagnosis, Pre; TITLE OF INVENTION: Diagnosis, PRITIE OF INVENTION: Diagnosis, PRITIE OF INVENTION: Histone HI NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LIP
STREET: 4370 La Jolla Village Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide LOCATION: 1..222
                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-041-889-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Sequence 32, Application US/09041889
Fatent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Microbial UC paNCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                     Gaps
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                                                                                       36.2%; Score 77; DB 3; Length 222;
52.2%; Pred. No. 0.15;
ive 1; Mismatches 13; Indels
                                                                                                                                                                                                                        118 AKPKAKKAGAAKAKKPAGATPKKAKKAAGAKKAVKKTPKKAKKPAA 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTOKNET AGENT INFORMATION:
NAME: Cambell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELEPHONE: (619) 555-9001
TELEPHONE: (619) 555-9001
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-08-152-488-13
; Sequence 13, Application US/08152488
; Patent No. 5534619
; GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 226 amino acids
amino acid
                                                                                         Query Match 36.2
Best Local Similarity 52.2
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-09-041-889-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Diego
STATE: California
COUNTRY: USA
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Gaps
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Sequence 13, Application US/08677304

Patent No. 5721212

GENERAL INFORMATION:

APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.

APPLICANT: Stanley, James C.

ITILE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL

NUMBER OF SEQUENCES: 13

CORRESPONDENCES. 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Benita J, Rohm, Esq.

STREE: 512 Springfield Avenue
CITY: Cranford

STATE: New Jersey

COMPUTRY: United States of America

ZIP: 07016-1811

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IRM PC Compatible

COMPUTER: NEW DOSS

SOFTWARE: WORGPERFECT 6; ASCII (DOS) Text
STATE: STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-441s.
COMPUTER: Michigan
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: IBM FC compartible
OPERATURG SYSTEM: MS-DOS v.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERENCE/ODCKET NUMBER: 7WH-060548-00231
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) DOCTOMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N/A
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Patent No. 5614494
GENERAL INFORMATION:
APPLICANT: Wakefield Thomas W.
APPLICANT: Andrews, Philip C.
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: MOWEL PEPTIDES FOR HEPARIN TITLE OF INVENTION: ADMINISTRATION AND TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
      James C.
NOVEL PEPTIDES FOR HEPARIN AND
LOW MOLECULAR WEIGHT HEPARIN
ANTICOAGULATION REVERSAL
                                                                                                                                                                                 ADDRESSEE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
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                      TITLE OF INVENTION: NOVEL PEPTIDES
TITLE OF INVENTION: LOW MOLECULAR W
TITLE OF INVENTION: ANTICOAGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE: N/A PUBLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 22; Conserve
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Gaps
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Pred. No. 0.038;
3; Mismatches 4; Indels
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Sequence 16, Application US/08303025

Patent No. 5614494

GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN AND TITLE OF INVENTION: ANTICOAGULATION REVERSAL, NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITALING Detroit
STATE: Michigan
COUNTY: Detroit
STATE: Michigan
COUNTY: United States of America
ZIP: 415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: IBM PC comparable
OPERATING SYSTEM: MS-DOS v. 6.22
SOFTWARE: WordPerfect 6:1; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIFICATION: 514
                 APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: ROIM, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/POCKET NUMBER: 7WK-060548-00233
TELEPHONE: 313-965-1996
TELEPHONE: 313-965-1996
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICE APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERNCE/DOCKET NUMBER: 7WH-060548-00231
TELEPHONE: 313-496-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AKKA-AKKAKKA-AKKAKKAAKKAKKAKKA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.0%;
68.8%;
                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 35.0
Best Local Similarity 68.8
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 313-496-8454 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
US-08-436-703B-2
PRIOR APPLICATION DATA:
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Patent No. 5919761
GENERAL INFORMATION
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: WEIGHT HEPAIN
TITLE OF INVENTION: WEIGHT HEPAIN
TITLE OF INVENTION: WEIGHT HEPAIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: Suite 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
            APPLICATION NUMBER: US/08/677,304
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 908-276-3344
TELEPAX: 908-276-543
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTER STICS:
LENGTH: 32 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: NO: 5721212 Relevant
TOPOLOGY: NO: 5721212 Relevant
MOLECULE TYPE: peptide
ORGANISM: NO' AMATION:
AUTHORS: N'A
AUTHORS: N'A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AKKA-AKKAKKA--AKKAKKAAKKAKKAAKKA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WordPerfect 6;
SOFTWARE: WordPerfect 6;
SOFTWARE: ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-677-304-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-436-703B-2
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2

us-09-816-989a-2.open.rai

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SEQUENCE CHARACTERISTICS:
LEXENTER 13 annino acide
TYPE: annino acide
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3;
                                                                                                                  35.0%; Score 74.5; DB 2; Length 33; 68.8%; Pred. No. 0.039; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                    5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
                                                                                                                                                                                                                        3 AKKA-AKKAKKA--AKKAKKAAKKAKKAAKKA 31
                                                                                                                                                                                                                                                                                                Search completed: March 10, 2003, 12:30:02 Job time: 8.97468 secs
                                                                                                                                      Best Local Similarity 68.89 Matches 22, Conservative
) ORGANISM: N/A
) PUBLICATION INFORMATION:
) AUTHORS: N/A
IS-08-436-703B-4
                                                                                                                      Query Match
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GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein March 10, 2003, 12:15:04; Search time 16.4219 Seconds (without alignments) 327.825 Million cell updates/sec Run on:

US-09-816-989A-3 266 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	tolA protein - Esc	hypothetical prote	-	membrane spanning	tola protein [impo	probable erythrocy	outer membrane int	histone H1 - sea u	TolA protein PA097	histone H1-beta, e	sperm tail-specifi	histone H1 - rainb	hypothetical prote	hypothetical prote		repetitive protein	outer membrane pro	histone H1-gamma,	histone H1, gonada	probable translati	Tola colicin impor	probable hupB - My	et	zuotin - yeast (Sa	kinase-like protei	histone H1 homolog	R27-2 protein - Tr	histone H1.10 - ch	histone H1 - wheat
SUMMARIES	OI	JV0057 '	AE1317	F90725	G85576	AG0592	T09127	G64064	A25550	E83525	A28100	S51364	HSTR1R	AE1689	T17698	809388	E60110	B43592	A26721	HSUR1P	T11583	AC0138	G70673	A44993	S25194	T48600	S61926	T30296	æ	S22322
	DB	7				~											~										~	~		
	Length	421	239	394	394	376	1701	372	210	347	211	1390	206	243	311	206	219	384	217	248	1403	388	214	328	433	703	182	1128	220	236
de	Query Match	44.0	43.8	42.5	42.5	41.5	41.4	39.7	38.5	38.5	38.3	37.8	37.4	37.0	37.0	36.7	36.5	36.1	35.9	35.9	35.9	35.7	35.5	35.5	35.3	35.3	34.8	34.8	34.6	34.6
	Score	117	116.5	113	113	110.5	110	105.5	102.5	102.5	102	100.5	99.5	98.5	98.5	97.5	97	96	95.5	95.5	95.5	95	94.5	94.5	94	94	٠	92.5	92	
	Result No.	н	~	m	4	Ŋ	9	7	60	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27		29

RESULT 2 AE1317

histone H1-delta - histone H1 (clone histone H1-TT - Vo	conserved hypothet IgA-specific metal	immediate-early pr translation initia	probable late embr histone H1 - trout	tolA protein VC183 arylesterase-relat	hypothetical prote hypothetical prote	histone H1 (clone hypothetical prote
A32137 T06241	E75383 A26039 S59589	EDBEQ3	T14305 HSTR1	A82152 G87675	T32633 T34010	T06257 T03561
01010	1000	140	7	N N	0 0	77
185 284 241	581 1532 231	407	136	356 438	1655	288 461
34.4 4.4.4	34.0	33.8	33.6	33.6 33.6	33.5	33.1
91.5	90.06 8.09	8 6 6	89.5	89.5 89.5	88.5	888
30 31	1 60 60 60 1 60 40 70	36	3 8 3 6 8 6	40	4 4 43	44 45

# ALIGNMENTS

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C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002
C;Accession: UV0057; B640-805
R;Levengood, S.K.; Webster, R.E.
J. Bacteriol. 171, 6600-6609, 1989
A;Title: Wuclectide sequences of the tolA and tolB genes and localization of their productive center and upper and upper production UV0057; WUID:90078104; PMID:2687247
                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-421 <LEV-
A;Cross-references: GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g148019
A;Experimental source: strain July
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
B;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A;Rose, D.J.; Mau, B.; Shao, Y.
A;Rose, D.J.; Mau, B.; Shao, Y.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64810
A;Status: nucleic acid sequence not shown; translation not shown
A;Status: 1-421 kBLAT
A;Residues: 1-421 kBLAT
A;Residues: 1-421 kBLAT
A;Residues: 1-421 kBLAT
A;Residues: GB:AB000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960;
A;Cross-references: GB:AB000177; cubstrain MG1655
C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach tl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
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44.0%; Score 117; DB 2; Length 421;
Best Local Similarity 54.7%; Pred. No. 0.0043;
Matches 35; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CiReywords: nucleotide binding; P-loop; transmembrane protein F;14-34/Domain: transmembrane #status predicted <MSS> F;78-301/Domain: helical #status predicted <HSR> F;35-362/Region: nucleotide-binding motif A (P-loop)
tolA protein - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 17 min
A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 RKKA 211
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Gaps

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98

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A;Cross-references: GB:AE005174; NID:gl2513672; PIDN:AAG55075.1; GSPDB:GN00145; UWGP:209
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: tolA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collaborated [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18 C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C; Accession: AG0592 R; Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A; Rtherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Attle: Complete genome sequence of a multiple drug resistant Salmonella enterica serove, A; Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable erythrocyte-binding protein MAEBL - Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Date: Il-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T09127
R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
Proc. Natl. Acad. Sci. U.S.A. 95, 1210-1215, 1998
A;Title: A family of chimeric erythrocyte binding proteins of malaria parasites.
A;Reference number: Z16577; MUID:98115903; PMID:9448314
A;Accession: T09127
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAYAKKAEKAAKKAFAKAYK-AAEAKKKAFA------KYKAEAAKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 EBARKKAAADAKKKAEAEAAKAAAEAQKKAEAAAALKKKAEAAEAAAAEARKKA 211
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C;Keywords: alternative splicing; cell binding; erythrocyte invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 376;
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                                                                                                                                                                                                                                                                                                                Length 394;
                                                                                                                                                                                                                                                                                                           Score 113; DB 2; Length 39
Pred. No. 0.0088;
5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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A;Residues: 1-1701 <KRB>
A;Cross-references: EMBL:AF031886; NID:92947227; PID:92947228
A;Experimental source: subspecies yoelii; strain YM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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llarity 53.5%; Pred. No. 0.014;
Conservative 5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 110; DB 2;
Pred. No. 0.047;
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0%;
Matches 33; Conservative
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54.2%;
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les 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Accession: AG0592
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-376 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                        A:Residues: 1-394
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Matches
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hypothetical protein Imo1941 [imported] - Listeria monocytogenes (strain EGD-e) (5) Esecies: Listeria monocytogenes (5) Esecies: Listeria (5) Esecies: Listeria (5) Esecies: Listeria (5) Esecies: Listeria (6) 
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: P90725
B;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Gasawara, N.; Vasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Stetus: preliminary
A;Stetus: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-239 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAD00019.1; PID:g16411394; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
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A; Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GN00154
A; Experimental source: strain 0157:H7, substrain RIMD 0509952
C; Genetics:
A; Gene: EC80774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 EKAYAKKAEKAAKKAEAKAYK-AAEAKKKAEA----KYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 43.8%; Score 116.5; DB 2; Length 239; 1. Similarity 55.4%; Pred. No. 0.0031; 31; Conservative 9; Mismatches 15; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 113; DB 2; Length 394;
Pred. No. 0.0088;
5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.5%;
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Matches 33; Conserv
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A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc
A;Reference number: A82950; MUID:20437337; PMID:10984043
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A;Experimental source: strain PA01
                                                                                                                                                                                                                                                           C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83525
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey,
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,
.; Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 28-Mug-1989 #sequence_revision 28-Mug-1989 #text_change 23-Feb-1997
C;Accession: A28100
R;Lai, Z.C.; Childs, G.
Mol. Cell. Biol. 8, 1842-1844, 1988
Mol. Cell. Biol. 8, 1842-1844, 1988
A;Title: Characterization of the structure and transcriptional patterns of A;Reference number: A28100; MUID:88246461; PMID:2837660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 ARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKRAEDEAKKKAAEDAKKKAAEDA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KKAEAKYKAEAAKAAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Keywords: chromosomal protein; DNA binding; embryo; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nistone H1-beta, embryonic - sea urchin (Strongylocentrotus purpuratus)
                                                                                                                                                                                                                                   Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sperm tail-specific protein mst101(2) - fruit fly (Drosophila hydei)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.3%; Score 102; DB 2; Length 211; 44.8%; Pred. No. 0.046; ive 5; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 102.5; DB 2;
Pred. No. 0.061;
7; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 KKKA--EAKYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKKAEAKA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 38.5%;
Best Local Similarity 43.0%;
Matches 37; Conservative
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Conservative
                                                                                                                                                                                                                                   Tola protein PA0971 [imported]
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                                                                                      156 PAKKAAKKPAAKKA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Superfamily: histone H1
                                43 EAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 30; Conserv
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A, Residues: '1-211 <LAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Residues: 1-347 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary A;Molecule type: DNA
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Matches
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histone H1 - sea urchin (Lytechinus pictus)
histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
C;Accession: A25550
R;Knowles, J.A.; Childs, G.J.
Rythowles, J.A.; Childs, G.J.
A) Worleic Acids Res. 14, 8121-8133, 1986
A;Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus an A;Reference number: A25550; MUID:87040778; PMID:3022245
                                                                                                                                                                                         RESULT 7
GG64064

GG64064

Outer membrane integrity protein tolA - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: G64064; JC5222
C;Accession: G64064; JC5222
R;Pielschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.P.; Kerlavage, R;Pielschmann, R.D.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weidman, J. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Aritle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; WUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 'V',2-47,'A',49-141,'R',143-164,'P',166-189,'R',191-202,'A',204-226,'A',228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U32722; GB:L42023; NID:g1573348; PIDN:AAC22041.1; PID:g1573353; R;Sen, K.; Sikkema, D.J.; Murphy, T.F. Gene 178, 75-81, 1996
A;Title: Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA A;Reference number: UC5212; MUID:97080550; PMID:8921895
A;Status: preliminary
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                                                                                         96 KTEAQKARAAAKKAKLAAKKKEQKEKKAAKTKARKEKLAAKKAAKKAAKKVKKPAAKAK 155
     Gaps
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                                                     5 AKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEA-----KYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:XO4488; NID:g9616; PIDN:CAA28177.1; PID:g9617
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:U32470
A;Experimental source: strain 1479
A;Note: the authors translated the codon CGT for residue 190 as Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-372 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 39.7%; Score 105.5; DB 2; Length 3 Best Local Similarity 48.2%; Pred. No. 0.036; Matches 27; Conservative 14; Mismatches 14; Indels
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  14; Indels
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Pred. No. 0.042;
5; Mismatches 1
Mismatches
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  5;
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41.9%;
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Best Local Similarity 41.9
Matches 31; Conservative
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: tolA
A;Start codon: GTG
32;
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Matches
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ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUD:21537279; PMID:11679669
A; Accession: AB1689
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-243 <GLA>
A; Cross-references: GB:AL592022; PIDN:CAC97285.1; PID:g16414556; GSPDB:GN00178
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Parechinus angulosus (angulate urchin)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S09388
R;Hill, C.S., Martin, S.R.; Thomas, J.O.
R;Hill, C.S., Martin, S.R.; Thomas, J.O.
A;Title: A stable alpha-helical element in the carboxy-terminal domain of free and chromany. A;Reference number: S09388; MUID: 90060019; PMID: 2583125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apportetical protein A208R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Accession: T17699 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T1769 #sequence_revision 15-Oct-1999
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Rcession: T17699
A;Accession: T17699
A;Accession: T17699
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KKYAKKEKAYAK-----KAEKAAKKAEAKAYKAAEAKK----KAEAKYKAEAAKAAAK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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43.9%; Pred. No. 0.12;
ive 8; Mismatches 18; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96576.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 36.7%; Score 97.5; DB 2; Length 2 1 Similarity 52.6%; Pred. No. 0.11; 30; Conservative 3; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 98.5; DB 2;
Pred. No. 0.1;
9; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            histone H1 - sea urchin (Parechinus angulosus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.0%;
50.0%;
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C, Superfamily: histone H1
C, Keywords: chromosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 50.03
Matches 28; Conservative
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Best Local Similarity 43.9
Matches 29; Conservative
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A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-206 <HIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-311 <GRA>
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S09388
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              C;Species: Drosophila hyde:
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S51564; S34154
C;Accession: S51564; S34154
R;Nesen, J.; Padmanabhan, S.; Buenemann, H.
Bur. J. Blochem. 225, 1089-1095, 1994
A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represe lpha-helical rods within the extremely elongated spermatozoa of Drosophila hydei.
A;Reference number: S51364; MUID:95045538; PMID:7957199
A;Accession: S51364
A;Status: nucleic acid sequence not shown
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A; Redidues: 1-206 cMEZ.
A; Residues: 1-206 cMEZ.
A; Cross-references: GB:XO2624; NID:g64323; PIDN:CAB37646.1; PID:g4468016
C; Superfamily: histone H1
C; Keywords: chromosomal protein; DNA binding; nucleosome
F;1-44/Region: flexible nose
F;45-117/Region: globular head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KKYAKKEK--AYAKKAEKAAKKAEAKAYK----AAEAKKKAEAKYKAEAAKAAAKEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-163, E', 164-236, 'Q', 237-254, 257-320, 'E', 321-1390 <NEW>
A; Cross-references: EMBL: X73481; NID: g313201; PID: g313202
A; Genetis:
A; Gene: mst101(2)
A; Cross-references: FlyBase: FBgn0011816
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0.074;
-hes 18; Indels
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Pred. No. 0.26;
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                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residudes: 1-1390 (NEE>
A; Cross-references: EMBL:X73481
R; Neesen, J.; Heinlein, U.A.O.; Buenemann, H.
submitted to the EMBL Data Library, June 1993
A; Reference number: S34153
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Matches 30; Conservative
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Mon Mar 10 13:08:09 2003

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Search completed: March 10, 2003, 12:28:27 Job time : 17.4219 secs

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# GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

March 10, 2003, 12:15:01 ; Search time 12.7595 Seconds
 (without alignments)
182.035 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-816-989A-3 266 1 AKKYAKKEKAYAKKAEKAAK......BAKYKAEAAKAAAKEAAYEA 56

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Q08695 drosophila P08284 gallus gall O86373 Rireptomyce P40276 chironomus P19549 treponema p Q02281 chlamydia t P02257 echinolampa P02987 gallus gall Q07134 chironomus Q9x009 streptomyce Q9rg15 bacteroides P10771 caenorhabdi
MST1_DROHY H101_CHICK DBHZ_STRCO H1B_CHITB TWPB_TREPA HCT1_CHLTR H1_CHICK H1_CHITH TOPI_STRCO RS16_BACTN H11_CABEL
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## ALIGNMENTS

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MEDLINE=95350630; PubMed=7542800;
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                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fransport; Protein transport; Bactericcin transport; Transmembrane;
                                                                             X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421.

MEDLINE=99332679; PubMed=10404600;
Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.;
Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.;
Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.;

"Filamentous phage infection: crystal structure of g3p in complex with its coreceptor, the C-terminal domain of Tola.";

Structure 7:711-722(1999).

-!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A COLICINS (COLICINS A, E1, E2, E3, AND K). NECESSARY FOR THE COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERIPLASMIC (POTENTIAL).
DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
             "TolA central domain interacts with Escherichia coli porins.";
EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.0%; Score 117; DB 1; Length 421; ilarity 54.7%; Pred. No. 0.0024; Conservative 5; Mismatches 10; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Inner membrane; 3D-structure; Complete proteome.
DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A(2,4).
8B2F52B4B97C655E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 AA; 43156 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M28232; AAA24683.1; -.
EMBL; AE000177; AAC73833.1; -.
EMBL; D90713; BAA35405.1; -.
PTR; JV0057; JV0057.
PDB; 1TOL; 20-MAX-99.
                                                                                                                                                                                                                                                                                              OF BACTERIOPHAGE DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; ITOL; 20-MAY-99.
EcoGene; EG11007; tolA.
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421
310
421
278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCB, TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tola protein.
Tola OR HI0383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 RKKA 211
                                                                                                                                                                                                                                                                                                                                   AND LAMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus.
Lloubes R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
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                                                                                                                                                                                                                                                                        "Whole-genome random sequencing and assembly of Haemophilus influenzae
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hamma M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Geoghagen N.S.M., Ghehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE=97080550; PubMed=8921895;
Sen K., Sikkema D.J., Murphy T.F.;
"Isolation and characterization of the Haemophilus influenzae tolQ,
tolR, tolA and tolB genes.";
Gene 178:75-81(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V -> A (IN STRAIN 1479).

K -> R (IN STRAIN 1479).

A -> P (IN STRAIN 1479).

A -> R (IN STRAIN 1479).

A -> A (IN STRAIN 1479).

V -> A (IN STRAIN 1479).

D -> A (IN STRAIN 1479).

A -> ARAAABRAKAR (IN STRAIN 1479).

T -> A (IN STRAIN 1479).

I -> F (IN STRAIN 1479).

I -> V (IN STRAIN 1479).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I -> V (IN STRAIN 1479).
N -> S (IN STRAIN 1479).
T -> A (IN STRAIN 1479).
S -> P (IN STRAIN 1479).
266ECF05C6C95544 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39831 MW;
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                                                                                                                                                                                                                                                                                                                                   Science 269:496-512(1995)
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TIGR; HI0383; -.
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27; Conserv
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RS6 AEDAL
ID RS6 AI
AC Q9076
DT 15-JU
DT 15-JU
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us-09-816-989a-3.open.rsp

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H1_LYTPI
P06144;
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ID_ H1_I
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Gavino V.H., Fallon A.M.;

Gavino V.H., Fallon A.M.;

Gavino V.H., Fallon A.M.;

Submitted (NAY-1999) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN CONTROLLING CELL GROWTH
AND PROLIFERATION THROUGH THE SELECTIVE TRANSLATION OF PARTICULAR
ALGSES OF MRNA (By similarity).

-1- PTM: Ribosomal protein 86 is the major substrate of protein

kinases in eukaryote ribosomes (By similarity).
                                                                                                                                                                                                                                                                                                                                   Gavino V.H., Fallon A.M.;
"Acdes mosquitoes tribosomal protein S6 cDNA.";
"Acdes mosquitoes tribosomal protein S6 cDNA.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN CONTROLLING CELL GROWTH
AND PROLIPERATION THROUGH THE SELECTIVE TRANSLATION OF PARTICULAR
CLASSES OF MRNA (By similarity).
-!- PTM: Ribosomal protein S6 is the major substrate of protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aedes aegypti (Yellowfever mosquito).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pteryguta; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Aedes.
NCBI_TaxID=7159;
                                                                                                Aedes albopictus (Forest day mosquito).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Aedes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKKYAKKE-KAYAKKAEKAAKKAEAKAYKA------AEAKKKA-----EAKYKA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinases in eukaryote ribosomes (By similarity).
SIMILARITY: BELONGS TO THE SGE FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribosomal protein; Phosphorylation.
SEQUENCE 349 AA; 39619 MW; 669A5DA33F8BADD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.5%; Score 105; DB 1;
46.5%; Pred. No. 0.02;
iive 7; Mismatches 13;
15-JUN-2002 (Rel. 41, Last annotation update) 40S ribosomal protein S6.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
405_ribosomal protein S6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD003460; Ribosomal S6E; 1. PROSITE; PS00578; RIBOSOMAL S6E; 1.
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Pfam; PF01092; Ribosomal S6e; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF154066; AAF04789.1; -.
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315 KAAPAAKKEA 325
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09U761;
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127 RS6 A

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                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels '15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----KAEAKYKAEAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lytechinus pictus (Painted sea urchin).
Bukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HISTORE #100778, PubMed=3022245;

Knowles J.A., Childs G.J.;

Nucleic Acids Res. 14:8121-8133(1986).

-! FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.

-! SUBCELLULAR LOCATION: Nuclear.

-! SIMILARITY: BELONGS TO THE HISTONE HI/H5 FAMILY.
-1- SIMILARITY: BELONGS TO THE S6E FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD003460; Ribosomal_S6E; 1.
PROSTE; PS00578; RIBOSOWAL_S6E; 1.
Ribosomal protein; Phosphorylations
SEQUENCE 346 AA; 39365 MW; 599CFF7B22BDBDFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.3%; Score 104.5; DB 1;
45.6%; Pred. No. 0.022;
tive 5; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKE-KAYAKKAEKAAKKAEAKAYKAAEAKK-
                                                                                                                                                                                                                                                                                                                                                        EMBL, AF154067; AAF04790.1; -. InterPro; IPR001377; Ribosomal S6E. Pfam; PF01092; Ribosomal S6e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P02259, 1HST.
InterPro; IRR001386; Histone H1/H5.
InterPro; IPR003116; Linkerhist N.
PFGM; PF00538; Linker histone; I.
ProDom; PD000373; Linkerhist N; I.
SMART; SM00526; H15; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X04488; CAA28177.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 45.6°
Matches 31, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A25550; A25550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 PAVAKKEA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAAAKEAA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Late histone H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Embryo;
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PERIPLASMIC (POTENTIAL)

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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

MEDLINE=20431337; PubMed=10984043;

MEDLINE=20431337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E. W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                   96 KTEAQKARAAAKKAKLAAKKKEQKEKKAAKTKARKEKLAAKKAAKKAAKKVKKPAAKAK 155
                                                                                                                      Gaps
                                                                                                                                                                   2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-------KKAEAKYKA 42
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 210 AA; 21746 MW; 08C38F64894007E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE004530; AAG04360.1; -.
Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                  Score 102.5; DB 1; Lens.
Pred. No. 0.022;
Pred. No. 0.19; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dennis J.J., Lafontaine E.R., Sokol P.A.; "Identification and characterization of the tolQRA genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           347 AA.
                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97113525; PubMed=8955385;
                                                                      38.5%;
41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U39558; AAC44660.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         opportunistic pathogen.";
                                                                                                                   31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS TO N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                     156 PAKKAAKKPAAKKA 169
                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                     43 EAAKAAAKEAAYEA
                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
OR PA0971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOLA PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=PAO;
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                         SEQUENCE
                                                                   Query Match
                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPERMATIDS.
DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
REPEATS.
                                                                                                                                                                                                                                         OF
                                                                                                                                                                                                            ----YKAAE-A 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meesen J., Padmanabhan S., Buenemann H.; Meesen J., Padmanabhan S., Buenemann H.; Marademly arranged repeats of a novel highly charged 16-amino-acid motific representing the major component of the sperm-tail-specific axoneme-associated protein family DhmstlO1 form extended alpha-helical rods within the extremely elongated spermatozoa of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Figure 1 Sperm; Repeat; Multigene family. Polymorphism.

Sperm; Repeat; Multigene family. Polymorphism.

332 1268 59 X 16 AA APPROXIMATE TANDEM REPEATS

SEQUENCE 1391 AA; 159000 MW; 1B2A368F30F48878 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKYAKKEK--AYAKKAEKAAKKAEAKAYK----AAEAKKKAEAKYKAEAAKAAAKEAA
                                                                                                                                                      31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila hydei.";

Eur. J. Blochem. 225:1089-1095(1994).

Eur. J. Blochem. 225:1089-1095(1994).

-! PUNCTION: POSSIBLE STRUCTURAL IN THE SPERM TAIL.

-! SUBCELLULAR LOCATION: Cytoplasmic.

-! SUBCELLULAR LOCATION: Cytoplasmic.

-! TISSUE SPECIFICITY: TESTIS. PRIMARY SPERMATOCYTES AND EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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                                                                                                      Length 347;
                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Indels
                                                   EEDD4B04AA095945 CRC64;
                                                                   Score 102.5; DB 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                     38.5%; Score 43.0%; Pred. No. 0.032,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Axonome-associated protein mst101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 100.5; DE Pred. No. 0.15; 4; Mismatches .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND CHARACTERIZATION. MEDLINE=95045538; PubMed=7957199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S34154; S34154.
FlyBase; FBgn0020733; Dhyd\mst101(2)
                                                                                                                                                                                                                                                                                                                                               180 KKKAAEEAKKKA-AAEAAKKKAAVEA 204
                                                                                                                                                                                                            1 AKKYAKKEKAYAKKAEKAAKKAEAKA----
                                                                                                                                                                                                                                                                                                                  33 KKKA--EAKYKAEAAKAAAKEAAYEA
                                                   37935 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila hydei (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.8%;
50.8%;
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                                                                                                                                                         37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
38 3
209 2
347 AA;
                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DROHY
                                                     SEQUENCE
                                                                                                        Query Match
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                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DROHY
                                                                                                                                                         Matches
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Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the Buropean Bioinformatics Institute of Endinformatics English outstation the Buropean Bioinformatics Institute of English on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chironomus tentans (Midge).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Chironomoidea; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKEKAYAKKAEK-----AAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAA 53
                                                                                                                                                                                                         Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schulze E., Wisniewski J.R., Nagel S., Gavenis K., Grossbach U.;
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=85564847; PubMed=6443128; MEZQLINE=85564847; PubMed=6443128; MeZquita J., Connor W., Winkfein R.J., Dixon G.H.; MeZquita J., Connor W., Winkfein R.J., Dixon G.H.; J. MoZ. D. 21:209-219 (1985).

-i. FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OF NUCLESOSME CHAINS INTO HIGHER ORDER STRUCTURES.

-i. SUBCELULAR LOCATION: Nuclear.

-i. SIMILARITY: BELONGS TO THE HISTONE HI/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 99.5; DB 1; Length 206;
Pred. No. 0.038;
7; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACETYLATION (BY SIMILARITY). GLOBULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72C440798066716C CRC64;
                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone HIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 AA.
                                                                                      206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, PO8287, IGHC.
InterPro, IPR001386, Histone H1/H5.
Pfam, PF00538; linker histone; 1.
ProDom; PD000373; Linkerhist N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20672 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X02624; CAB37646.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Uner, ...
Best Local Similari,
Watches 28; Conservative
                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 AA;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acetylation.
INIT MET
MOD RES
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                                                                                   H1 ONCMY P06350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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DT 01-FE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>~</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 AKKATKAAKPAAKKVAAKPAAKKAAAPKPKAAAKPKKEVKPKKEAKPKKAAAKPAKA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003186; Linkerhist N.
Pfam; PF00538; linker histone; I.
ProDom; PD000373; Linkerhist_N; I.
SWART; SW0526; H15; I.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 237 AA; 24689 WW; D429364FFBCB1F3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYAKK--AEKAAKKAEAKAYKAA----EAKKKAEAKYKAEAAKAAAKEAA 53
-i- FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OF NUCLEDSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: BELONGS TO THE HISTONE HI/HS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1-beta, late embryonic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L29105; AAB53945.1; -. HSSP; P08287; 1GHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M20314; AAA30052.1; -. PIR; A28100; A28100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 KPA 228
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DOMAIN
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                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              from Mycobacterium.",
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK------KKAEAKYKAEAAKAAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prabhakar S., Tyagi J.S., Prasad H.K.; "HLPMt-A target for differentiation of M.tuberculosis and M.bovis."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      Chromosomal protein, Nuclear protein, DNA-binding, Multigene family. SEQUENCE 211 AA, 22169 MW, 9F214581334BBE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matsumoto S., Yukitake H., Matsuo T., Mineda T., Yamada T., "Identification of a novel protein generating bacterial slow growth
                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9XB18; 09S5J5; 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (HIP).
                                                                                                                                                                                                                                                                                 37.2%; Score 99; DB 1; Length 211; 44.8%; Pred. No. 0.042; tive 4; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                               21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 AA.
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DNA-bindwng; DNA condensation; Repeat.
                          InterPro; IPR001386; Histone H1/H5. InterPro; IPR003216; Linkerhist N. Prems, PF00538; Linker histone; T. ProDom; P0000173; Linkerhist N; I. SWART; SM00526; H15; I. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR00119; Bac DNAbind.
InterPro; IPR00119; Bac DNAbind.
Pfam; PF00216; Bac DNA binding; 1.
ProPom; PR00624; HISTONEH5.
ProPom; PD000045; Bac DNAbind; 1.
SWART; SM00411; BHL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, Y18421, CAB46493.1, -.
EMBL, AB013441, BAA78330.1, -.
HSSP, P02346, 1HUU.
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BCG / Tokyo;
                                                                                                                                                                                                                                                                                                               Local Similarity
tes 30; Conserv
HSSP; P02259; 1HST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=AN5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DBH MYCBO
                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                  Matches
셤
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1-11.
1-13.
1-14.
1-15.
1-16.
1-17.
6 X 8 AA TANDEM REPEATS OF [EA]-A-A-R-X-
                                                                                                                                                                                                                                                                                                                              Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell F., Sliviensky L., Schouls L.M., van Embden J.D., Charon N.W.;
"Treponema phagedenis encodes and expresses homologs of the Treponema pallidum TmpA and TmpB proteins.";
Infect. Immun. 59:3685-3693(1991).
-!- FUNCTION: TMP MAX SERVE AS A PORIN OR TRANSPORT PROTEIN FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
TREPONEMAL MEMBRANE PROTEIN B.
17 X 5 AA TANDEM REPEATS OF K-A-A-[AKR]-
[ED].
                                                                             Gaps
                                                                           3;
                                                    Score 97.5; DB 1; Length 205; Pred. No. 0.055; Mismatches 15; Indels
                                                                                                                   111 AKKVAK--KAPAKKATKAAKKAATKA-PAKKAATKAPAKKAVKATKSPAKK 158
                                                                                                  2
 BACTERIAL HISTONE-LIKE DOMAIN
                                                                                                  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKE
           DEGENERATE REPEATS REGION
A -> T (IN REF. 2).
19FCE67885DFE6A8 CRC64;
                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Treponemal membrane protein B precursor (Antigen tmpB)
                                                                                                                                                                                                                                                  iner.
Treponema phagedenis.
Bacteria, Spirochaetales, Spirochaetaceae, Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: OUTER MEMBRANE-ASSOCIATED.
-1- SIMILARITY: TO TMPB OF T.PALLIDUM.
                                               36.7%; Score . 0.055; 56.9%; Pred. No. 0.055; 11.00 4; Mismatches 1
                                                                                                                                                                            384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen; Outer membrane; Repeat; Signal.
                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-1.
1-2.
1-3.
1-5.
                                                                                                                                                                                                                                                                                                           STRAIN=Kazan 5;
MEDLINE=91372983; PubMed=1894368;
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. 9
90 BA
205 DE
199 A
21262 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M58563; AAA27480.1; -. PIR; B43592; B43592.
                                                                 Local Similarity 56.9
nes 29, Conservative
                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
101
199
1
                                                                                                                                                                                                                                                                                                                                                                                                LARGE MOLECULES.
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          NCBI_TaxID=162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
151
                                                                                                                                                                           TMPB TREPH
P29720;
           DOMAIN
CONFLICT
SEQUENCE
                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
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REPEAT
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REPEAT
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DOMAIN
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STANDARD;
                                             195 KKAAKPAKKAA 205
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                         42 AEAAKAAAKEA
                                                                                                                                                                                                                                               SEOUENCE OF 1-84
                                                                                                                                                                                                                        NCBI_TaxID=7658;
                                                                                                                                                                                                              Parechinus.
                                                                                          HI_PARAN
ID_ HI_PARAN
AC__P02256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                 RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-87172742; PubMed=3031476; Knowles J.A., Lai Z.-C., Childs G.J.; "Isolation, characterization, and expression of the gene encoding the late histone subtype HI-gamma of the sea urchin Strongylocentrotus
                                                                                                                                                                Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                   1 AKKYAKKEKAYAKKA--EKAAKK--AEAKAYKAAEAKKKA----EAKYKAEAAKAAAKEA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chromosomal protein, Nuclear protein, DNA-binding, Multigene family. SEQUENCE 217 AA; 22658 MW; C7251EED3413B185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               purpuratus.";
Mol. Cell. Biol. 7:478-485(1987).
-!- FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE HI/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 35.9%; Score 95.5; DB 1; Length 217;
1 Similarity 43.7%; Pred. No. 0.084;
31; Conservative 5; Mismatches 16; Indels 19;
                                                                                                     DB 1; Length 384;
                                                                                                                             17; Indels
                                                                                 6E94CBC74294DE8C CRC64;
                                                                                                                                                                                                                                                                                                   01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1-gamma, late.
                                                                                                     Score 96; DB 1;
Pred. No. 0.12;
6; Mismatches
                                                                                                                                                                                                                                                                                 217 AA
                                                                                                                                                                                                                                                                                 PRT;
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InterPro; 1FR001386; Histone H1/H5.
InterPro; 1PR003216; Linkerhist N.
Pfam; PF00538; linker_histone; I.
  A-A-E
              ProDom; PD000373; Linkerhist N; 1.
                                                                                 42677 MW;
                                                                                                     Query Match
36.1%;
Best Local Similarity 51.6%;
Matches 33; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M16033; AAA30059.1; -.
                                                                                                                                                                                                                                                                                STANDARD;
             243
252
261
270
279
288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        Strongylocentrotus.
NCBI_TaxID=7668;
                                                                              384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
            236
245
254
254
263
272
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MEDLINE-80156832; PubMed=7363905;
Strickland W.N., Strickland M., Brandt W.F., von Holt C., Lehmann A., Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                       "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 1. Chemical and enzymatic fragmentation of the protein and the sequence of amino acids in the four N-terminal cyanogen bromde peptides."; Eur. J. Biochem. 104:559-566(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 35.9%; Score 95.5; DB 1; Length 248; Best Local Similarity 52.9%; Pred. No. 0.093; Matches 27; Conservative 4; Mismatches 19; Indels
                                                                                                               Histone H1, gonadal. (Angulate sea urchin).
Barechinus angulosus (Angulate sea urchin).
Bukaryota; Merezoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Buechinoidea; Echinacea; Echinoida; Echinidae;
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                                                                                                                                                                                                                                                                                              MEDLINE-80156831, PubMed-6767609;
Strickland W.N., Strickland M., de Groot P.C., von Holt C.,
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 K -> R.
26387 MW; 1B25B3F136541947 CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-CT-10TN-2002 (Rel. 41, Last annotation update)
Probable eukaryotic initiation factor C17C9.03.
                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
248 AA.
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YDF3 SCHPO
ID YDF3 SCHPO
AC Q10475;
DT 01-OCT-1996
DT 15-JUN-2002
DE Probable euk
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us-09-816-989a-3.open.rsp

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RA Wood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,
RA Wood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,
By Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Comnor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Collins M., Comnor R., Cronin N., Harris D., Hidalgo J., Hodgson G.,
A Holroyd S., Hornby T., Howarth S., Huche B.J., Hunt S., Jagels K.,
A Holroyd S., Wongel M., Leather S., McDonald S., McLean J.,
A Junes K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
A Juner K., O'Neil S., Pearson D., Quali M.A., Rabbinowitsch E.,
A Noney P., Moule S., Mungall K., Murphy E., Niblett D., Odell J.,
A Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
A Taylor K., Taylor R., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
A Taylor K., Langer E., Iseger M., Schaefer M., Mueller-Auer S.,
A Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Ber P., Zimmermann W., Wedler E., Mowerl D., Hilbert B.,
A Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
A Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
A Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
A Shapkovski G.V., Ussery D., Barrell B.G., Nurse P.;
A Shapkovski G.V., Ussery D., Barrell B.G., Nurse P.;
A Nature 415:871-880(2002)
A Nan D., Ann D., A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Initiation factor; Protein biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.9%; Score 95.5; DB 1; Length 1403; 44.3%; Pred. No. 0.38; 17; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1403 AA; 154034 MW; 0317EE65BE2A1E63 CRC64;
                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                   STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z73099; CAA97349.1; -. InterPro; IPR003890; IF_EIF4G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 44.3*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00543; MIF4G;
                                                                                                        Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA-binding.
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Search completed: March 10, 2003, 12:17:09 Job time : 13.7595 secs 625 A 625

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

March 10, 2003, 12:15:01 ; Search time 29.654 Seconds
 (without alignments)
 389.109 Million cell updates/sec

US-09-816-989A-3

266 1 AKKYAKKEKAYAKKAEKAAK......EAKYKAEAAKAAAKEAAYEA 56 Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

671580 segs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mammal:\*
sp\_phage:\*
sp\_phage:\*
sp\_plant:\*
sp\_rodent:\*
sp\_vortebrate:\*
sp\_vortebrate:\* SPTREMBL 10: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Q9wwx1 pseudomonas	Q9cm70 pasteurella	Q8y5w4 listeria mo	Q937k4 erwinia chr	Q8zqt6 salmonella	Q8x965 escherichia	093946 candida alb	Q8z8cl salmonella	O61164 plasmodium	Q8t5c8 plasmodium	Q8xvn7 ralstonia s	Q92a67 listeria in	Q84528 paramecium	Q9ndi9 plasmodium	Q9uv33 ascobolus i	Q9kj98 escherichia
SUMMAKIES			QI	Q9WWX1	Q9CM70	Q8Y5W4	Q937K4	Q8ZQT6	Q8X965	093946	Q8Z8C1	061164	Q8T5C8	Q8XVN7	Q92A67	084528	610N6Q	Q9UV33	Q9KJ98
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			Match Length DB	372	389	239	395	407	394	212	376	1701	1866	200	243	311	696	213	629
	ф	Query	Match	44.0	44.0	43.8	43.0	42.7	42.5	41.7	41.5	41.4	39.3	37.8	37.0	37.0	36.8	36.1	35.9
			Score	117	117	116.5	114.5	113.5	113	111	110.5	110	104.5	100.5	98.5	98.5	86	96	95.5
		Result	No.	н	7	m	4	2	9	7	80	6	10	11	12	13	14	15	16

Q9xh19 triticum ae Q8222 yersinia pe Q9y1p8 plasmodium O46141 mytilus edu O46142 mytilus edu O46362 mytilus edu O46362 mytilus edu O46362 mytilus edu O91ya2 arabidopsis Q99467 thizobium 1 O01395 drosophila Q93y66 arabidopsis Q45370 bordetella Q26947 trypanosoma Q865C9 plasmodium Q18319 chironomus Q21564 streptococc Q91566 streptococc Q91565 streptococc Q91567 plasmodium O98w3 triticum ae	triticum triticum triticum mytilus ec deinococc oryza sat leishmania ralstonia daucus ca
10 Q9XHL9 16 Q8ZGZZ 5 Q9Y1P8 5 Q9Y1P8 6 Q6141 5 O46143 10 Q91YA2 10 Q91XA2 10 Q91XA3 1	10 055794 10 055794 5 046140 10 09FP71 5 09BMY8 16 039YIF6 10 0336R10
275 388 848 848 191 191 191 134 137 1182 1182 1118 233 243 243 243 243 243 243 243 243 243	2223 2233 233 241 241 250 250 250 250 250 250 250 250 250 250
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## ALIGNMENTS

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MEDLINE=96198174; PubMed=8626299;
MEDLINE=96198174; PubMed=8626299;
RODINE=961982174., Ramos Gonzalez M.I., Ramos J.;
Rodinguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.;
Inpoprotein (PAL) is involved in maintenance of the integrity of the cell envelope.";
J. Bacteriol. 178:1699-1706(1996).
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96422022; PubMed=8824639;
Rodriquez-Herva U.J., Ramos U.;
Rodraccterization of an OprL null mutant of Pseudomonas putida.";
J. Bacteriol. 178:5836-5840(1996).
                                                                                                                                                                                                                                                                                                                                            Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                             372 AA.
                                                                         PRT;
                                                                             PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN=MT-2;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=303;
                                                                                                                                                                                                                                                                          Tola protein.
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                                                                         Q9WWX1
RESULT 1
                                    Q9WWX1
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32; Conservative
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Q937K4;
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Matches
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STRATE=EGD-E / SEROVAR 1/2A;
MEDLINE=21537279; PubMed=11679669;
MEDLINE=21537279; PubMed=11679669;
MEDLINE=21537279; PubMed=11679669;
MEDLINE=21537279; PubMed=11679669;
MEDLINE=21537279; PubMed E., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charghit A., Chetowani F., Couve E., de Dartvar A., Deboux P.,
Charghit A., Dominquez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
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Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006136; AAK03052.1;
HSSP; P19934; 1TOL.
InterPro; IPR000533; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
NCBI_TaxID=1639;
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                                                                                                   Score 117; DB 2; Length 372;
Pred. No. 0.0035;
2; Mismatches 12; Indels
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                                                            40133 MW; 87F49785ECC3C0BC CRC64;
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Last annotation update)
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein lmo1941.
                                                                                                                                                                                                                                                                                                                                        389 AA
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EMBL; X74218; CAB50780.1; -.
InterPro; IPR001386; Histone_H1/H5.
PRINTS; PR00624; HISTONEH5.
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MEDLINE=21145866; PubMed=11248100;
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                                                                                  Query Match
Best Local Similarity 66.0%
The 31; Conservative
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Best Local Similarity 55.9°
Matches 33; Conservative
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                                                              372 AA;
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Complete proteome.
SEQUENCE 389 AA;
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                                      PRINTS; PI
SEQUENCE
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SEQUENCE FROM N.A.
STRAIN=LT2 / SGSS1412 / ATCC 700720;
MEDILINE=1534948; PubMed=11677609;
MCDilland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
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Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordaiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R. Varguez-Boland J.-Rose M., Schlueter T., Simoes N., Tierrez A., Varguez-Boland J.-A., Voss H., Wehland J., Cossart P.; Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Pectobacterium.
NCBI_TaxID=556;
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                                                                                                                                                                         Science 294:849-852(2001).
BMBL; AL591901; CAD00019.1; -.
ListiList; LM001941; -.
InterPro; IPR002482; LysM.
Pfam; PF01476; LysM; 1.
SMART; SM00257; LysM; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 239 AA; 25836 MW; 72E59D576E0D7832 CRC64;
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Last annotation update)
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TOLA OR STM0747.
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
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SEQUENCE
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MEDLINE-21156231; PubMed-11258796;

MEDLINE-21156231; PubMed-11258796;

MEDLINE-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

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DNA Res. 8:11-22(2001).

EMBL; AR005253; AAG55075.1; -.

EMBL; AR005253; BAB34197.1; -.

InterPro; IPR000104; Antifreeze_1.
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MEDLINE=21074935; PubMed=11206551;

MEDLINE=21074935; PubMed=11206551;

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grobbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.",
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Escherichia.
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49.3%; Pred. No. 0.0079;
ive 10; Mismatches 9;
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InterPro; IPR000104; Antifreeze 1.
PRINTS; PR00308; ANTIFREEZEI.
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hes 37; Conservative
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Matches 33; Conserva
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                   157 EEAAKKAAADAKKKAEAEAAKAAAEAQKKAEAAAAALKKKAEAAEAAAAEARKKA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ascomycota; Saccharomycotina; Saccharomycetes;
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   ----KYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.7%; Score 111; DB 3; Length 212;
55.9%; Pred. No. 0.0071;
cive 5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaiser B., Kunkel W., Saluz H.P., Munder T.,
"Identification of Candida albicans protein domains with
transcriptional activating properties in Saccharomyces cs
Submitted (UNI-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ006637, CAA07165.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Fungi, Ascomycota, Saccharomycotina, Sacularos
Saccharomycetales, mitosporic Saccharomycetales, Candida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 AA; 38804 MW; EC21F2C4767A8A42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 AA; 24231 MW; 10C2122E9554A387 CRC64;
                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                     212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 AA
EKAYAKKAEKAAKKAEAKAYK-AAEAKKKAEA-
                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 413:848-852(201).
EMBL; AL627268; CAD05209.1; -
Interpro; IPR000104; Antifreezel.
PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01574; TUBBYPROTEIN.
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01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                       Candida albicans (Yeast).
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                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                   CTA2p (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=601;
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MEDLINE=21681879; PubMed=11823852;

MEDLINE=21681879; PubMed=11823852;

A salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

A ralat M., Billault A., Brottler P., Camus J.C., Cattolico L.,

Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,

A Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,

A Gaspin C., Lavie M., Malen M., Wincker P., Levy M.,

Melsenbach J., Boucher C.A.,

Melsenbach J., Boucher J.,

Melsenbach J., Melsenbach J.,

Melsenbach J., Boucher J.,

Melsenbach J., Boucher J.,

Melsenb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 AAKKAPAKKAVAKKAAPVAKKAPAKKVAAKKAPAAKKAPAAKKAAAVKKVAAKKAA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 200;
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Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, beta subdivision, Ralstonia group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.8%; Score 100.5; DB 16; Length
53.7%; Pred. No. 0.058;
ive 3; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 AA; 19279 MW; D3831B590510272D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Probable histone H1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein lin2055.
                                                                                                                                                                                                                                                                                                                                     200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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STRAIN=CLIP 11262 / SEROVAR 6A;
PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Conservative
                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listeria innocua.
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                                                                                                                                                     1514 A 1514
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                                                                            52 A 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                     Q8XVN7
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                                                                                                                                                                                                                                                                RESULT 11
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                                                                                                                                                                                                                                                                                                   Q8XVN7
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7
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                                                                                                                                                                                               Gaps
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                                                                                                                                                 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAEA------KYKAEAAKAA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEA-----KYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Evolutionary relationships of conserved cysteine-rich motifs in adhesive molecules of malaria parasites."; Mol. Brol. Evol. 0:0-0(2002). EMBL, AV042083; AALIO508.1; -. SEQUENCE 1866 AA; 212420 MW; DC692D7CFAE7D93F CRC64;
                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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ch 41.5%; Score 110.5; DB 16; Length 376; 1 Similarity 53.5%; Pred. No. 0.014; 38; Conservative 5; Mismatches 11; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=YM,
MEDLINE=98115903; PubMed=9448314;
MEDLINE=98115903; PubMed=9448314;
Kappe S.H.I., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.;
A family of chimeric erythrocyte binding proteins of malaria parasites.";
Proc. Natl. Acad. Sci. U.S.A. 95:1230-1235(1998).
EMBL, AR01886; AACO5366.1; -.
SEQUENCE 1701 AA; 199268 MW; EDA8EZDEFD87CE8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.4%; Score 110; DB 5; Length 1701; 54.2%; Pred. No. 0.064; ive 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium vivax.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKAYAKKAEKAAKKAEA--KAYKA--AEAKKKAEAKYKAEAAKAA
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=SALVADOR;
Michon P., Stevens J.R., Kaneko O., Adams J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1701 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1866 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erythrocyte binding protein. MAEBL.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 07,
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Best Local Similarity 55.73
Matches, 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium yoelii yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    201 ADAKKKADAEA 211
                                                                                                                                                                                                                                                                                               49 A---KEAAYEA 56
                                  Best Local Similarity
Matches 38; Conserv
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NCBI_TaxID=73239;
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01-OCT-2000
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AC 0875CB
DT 01-JUJ
DT 01-JUJ
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CO EUKAR
OX NCBI
RN NCBI
RN SEQUE
RA MICHO
RT AGHES
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SEQUENCE FROM N.A.
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Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.; Comparative genomics of Listeria species."; Science 294:849-852(2001).
EMBL, ALS64170; CAC97285.1; -. ListList; LIN02055; -. ListListCompletical protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=20478054; PubMed=11021991;
MEDLINE=20478054; Adams B.J., Graves M.V., Van Etten J.L.;
"Characterization of a beta-1,3-glucanase encoded by chlorella virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20013326; PubMed=10544099; Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W., Lisec A.D., Nickerson K.W., Van Etten J.L.; "R." Nickerson K.W." Van Etten J.L.; "Chlorella virus PBCV-1 encodes a functional homospermidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96187795; PubMed=8614977;
Lu Z., Li Y., Que Q., Kutish G.F., Rock D.L., Van Etten J.L.;
"Analysis of 94 kb of the chlorella virus PBCV-1 330-kb genome: map
positions 88 to 182.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
VCBI_TaxID=10506;
                                                                                                                                                                                                                                                                                                                                                                                                                                             37.0%; Score 98.5; DB 16; Length 243; ilarity 50.0%; Pred. No. 0.1; Conservative 9; Mismatches 18; Indels 1;
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Graves M.V., Van Etten J.L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
[8]
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                                                                                                                                                                                                                                                11 protein; Complete proteome.
243 AA; 25963 MW; 6B2493D143B159D1 CRC64;
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Submitted (DEC-1995)
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Matches 28; Conserv
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Galinski M.R., Ingravallo P., Corredor-Medina C., Al-Khedery B.,
Galinski M.R., Ingravallo P., Corredor-Medina C., Al-Khedery B.,
Povoa M., Barnwell J.M.;
"Plasmodium vivax merczóte surface proteins-3beta and-3gamma share
structural similarities with P. vivax merczóite surface protein-3alpha
and define a new gene family.";
Mol. Biochem. Parasitol. 115:41-53 (2001).
EMBL, AF099663; AAF78288.1;
SEQUENCE 969 AA, 104674 MW; 9AISOCCA9918FF77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  KKYAKKEKAYAK-----KAEKAAKKAEAKAYKAABAKK----KAEAKYKAEAAKAAAK 50
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                                                                                                                                                                                                                                                 Length 311;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=31273;
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                                                                                    Gurnon J.R., Graves M.V., Van Etten J.L.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
EMBL, U42580; AAC96576.1; -.
InterPro; IPR02048; BF-hand.
PROSITE; PS00018; BF-hand.
PROSITE; PS00018; BF-HAND; UNKNOWN 1.
Graves M.V., Van Etten J.L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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43.9%; Pred. No. 0.13;
ive 8; Mismatches 18;
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nes 29; Conservative
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tes 26; Conserv
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SEQUENCE FROM N.A.
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WEDLINE=20063166; PubMed=10594009;

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MEDLINE=20063166; PubMed=10594009;

MEDLINE=20063166; PubMed=10594009;

MEDLINE 1. Resident Messential For long life span.";

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Mel. Cell. Biol. 20:61-69(2000).

REMEL; AF190622; AAF16011.1; -..

REMEL; AF190622; AAF16011.1; -..

REMEL; AF19063136; Linker Histone HI/H5.

RICEPPO: IPRO002186; Linker Histone, I.

PRINTE; PRO00524; HISTONEHS.

PPODON; PD000373; Linker Histone, I.

REMEL; SM00526; HIS; 1.

REMEL; SM00526; HIS; 1.

SMART; SM00526; HIS; 1.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes;
Pezizales; Ascobolaceae; Ascobolus.
NCBI_TaxID=5191;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
36.1%; Score 96; DB 3; Length 213;
Best Local Similarity 44.8%; Pred. No. 0.15;
Matches 30; Conservative 4; Mismatches 17; Indels
                                                                                  SEQUENCE FROM N.A.
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16; Gaps

94 KLAKKEKAAAAPKKPAAKKAAAPKKDAAPKKAAAPKKAAAAPKSAAAKKTLIDAKKAAAKK 153

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3 KYAKKEKAYAKKAEKAAKKA-----BAKAYKAAEAKKKAEAKYKAEAAK 46

Search completed: March 10, 2003, 12:25:55 Job time : 30.654 secs

|||:|| 154 PAAKKAA 160 47 AAAKEAA 53

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 10, 2003, 12:15:01; Search time 29.1814 Seconds (without alignments) 255.712 Million cell updates/sec Run on:

US-09-816-989A-3 266

score: Perfect

1 AKKYAKKEKAYAKKAEKAAK.......EAKYKAEAAKAAAKEAAYEA 56 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

908470

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Copolymer molecula	Listeria monocytog	Recombinant copoly	Copolymer molecula	Peptide #10 used i					
ΩI	AAY82573	AAY82575	AAY82576	AAY82574	AAY82577	AAY82572	ABB49123	AAR06446	AAY82571	AAY98499
DB	21	21	21	21	21	21	23	11	21	21
% Query re Match Length DB I	99	77	86	99	109	45	239	106	35	100
& Query Match	100.0	92.3	87.6	74.4	67.9	50.6	43.8	41.7	39.3	39.1
Score	266	245.5	233	198	180.5	134.5	116.5	111	104.5	104
Result No.	н	7	e	4	2	9	7	ω	6	10

Amino acid polymer Poly-Lys-Ala used Nucleic acid trans	Recombinant copoly Amino acid sequenc Human protein semi	Plasmon Froctin Serve Plasmodium yoelii	Mycobacterium bovi		Zuotin. Saccharom	Human zuotin prote	S cerevisiae apopt	Nucleic acid (NA)	()	Trypanosoma cruzi	Trypanosoma cruzi	Neisseria IgA-Prot	Novel human diagno	High affinity macr	Human DNA modifica	Human protein sequ	Human protein sequ	E		Ø	Arabidopsis thalia	Synthetic helical	PspC alpha-helix c	Streptococcus pneu	S. pneumoniae PspC	Quail H1 histone p	Human ORFX protein
21 AAY59044 22 AAU04289 22 AAB45852	11 AAR06445 20 AAY14928 22 AAM25508	4 11 0				0	22 AAG70739				16 AAR84565	9 AAP80136	22 ABG28693	m	22 AAU03592				21 AAG36673	21 AAG36672	21 AAG36671		20 AAY43392	18 AAW14593	20 AAY43384	21 AAY76981	23 ABP00299
1000	154 223 146	1507	205	214	433	433	433	4 6	643	472	564	741	334	46	279	467	198	3502	494	521	620	140	589	929	929	219	111
39.1	38.7	38.0	36.7	35.5	35.3	35.3	35.3	35.5	4	4	34.4	34.0	33.8	33.6	33.6	•	33.3	33.3	•					32.1			31.8
104	103	101	97.5		94	94	4. 2	η.	92.5			90.5	90	89.5	89.5	89.5	88.5		87.5	87.5	87.5	86	85.5	85.5	85.5	85	84.5
122	15 15	17	966	212	22	23	24	2 2	27	28	59	30		32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

AAY82573 standard; peptide; 56 AA RESULT 1 AAY82573

AAY82573;

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronif immune thrombocytopeania purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; permphigus vulgaris; systemic lupus erythematosus.

Unidentified

WO200018794-A1

06-APR-2000

99WO-US22402 24-SEP-1999; 

98US-0101693. 25-SEP-1998; (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatinamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or treating and preventing immune either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple selevability inflamment ophoritis, autoimmune thyroiditis, autoimmune baemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune cuveorethnitis, Crohn's disease, chronic immune thrombocytopaenia pravis, contact sensitivity disease, diabetes mellitus, Graves disease, quillain-Barre's syndrome, Hashimoco's disease, and indopathic myxoedema, myasthenia gravis, psyndrome, Hashimoco's disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to molecular weights markers them ideal for use as
                                                                                                                             Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                          Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   molecular weight, markers.
                                                                            WPI; 2000-317499/27.
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                           Gad A,
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Gaps ö 100.0%; Score 266; DB 21; Length 56; 100.0%; Pred. No. 3e-20; ive 0; Mismatches 0; Indels Local Similarity 100. tes 56; Conservative Query Match Matches

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AAY82575 standard; peptide; 77 AA. AAY82575; RESULT 2

(first entry) 28-JUL-2000 Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Hashimoto's disease; idiopathic myxoedema, myasthenia gravis, pemphigus vulgaris; systemic lupus erythematosus. 

WO200018794-A1.

06-APR-2000.

99WO-US22402. 24-SEP-1999;

98US-0101693. 25-SEP-1998;

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC. (TEVA-)

Gad A,

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides (I) for determining the molecular convention describes polypeptides (I) for determining the molecular weight and an amino acid composition corresponding to the copolymer. The colypeptides of the invention are used as molecular weight markers for colypeptides of the invention are used as molecular weight markers for colypeptides of the invention are used as molecular weight markers for collegases which may be treated include either cell-mediated or troinemune complements and include either cell-mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple conditions, classases which may be treated include arthritic conditions, cancens, rheumatoid arthritis, outcommune thyroidities, autoimmune comporties and sense in an antibody-mediated disease, chronic immune thrombocytopaenia uncommune cophoritis, autoimmune thrombocytopaenia cuvecretinitis, contact sensitivity disease, diabetes mellitus, Graves CC disease, Guillain-Barre's syndrome, Hashimoto's disease, milain-Barre's syndrome, Hashimoto's disease, and mysathenia gravis, psoridated disease, and collises, e.g. mysoedema, mysathenia gravis, psoridated disease, and collises, e.g. mysoedema, mysathenia gravis, psoridated disease, and defined molecular weights and physical properties which are analogous to collise and physical properties which are analogous to collise and physical properties which makes them ideal for use as molecular weight markers.

77 AA; Sequence

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0; Indels 21; Gaps 92.3%; Score 245.5; DB 21; Length 77; 72.7%; Pred. No. 4.9e-18; ive 0; Mismatches 0; Indels 21; 56; Conservative Similarity Query Match Best Local S Matches

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40 YKAEAAKAAAKEAAYEA 56 61 YKAEAAKAAKEAAYEA 77 ઠે

AAY82576 standard; peptide; 86 AA. **AAY82576** 

AAY82576;

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

glatitamer accate; autoimmune disease, antiarthritic; neuroprotective, osteopathic; immunosuppressive, antithyroid; antinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; draves disease; dulllain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Copolymer; molecular weight marker; TV-marker; immune disease; 

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Copolymer, molecular weight marker; TV-marker; immune disease;
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                                                                                                                                                                                                                                      25-SEP-1998;
                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                          weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight on a main acid composition corresponding to the copolymer. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell mediated or antibody-mediated diseases. Such diseases include archritic conditions, cancerns, theumatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, ostecarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves (isease, Gillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and celined molecular weights and physpical properties which are analogous to glatizamer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                  AAY82571 to AAY82577 represent specifically claimed copolymer molecular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 86;
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 pemphigus vulgaris; systemic lupus erythematosus.
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Pred. No. 1e-16;
2; Mismatches
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                                                                                                                                                                                                                                                                          Claim 10; Page 14; 72pp; English.
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                                                                                                                                               YEDA RES & DEV CO LTD.
TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.6%;
62.8%;
                                                                                                                         98US-0101693.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecular weight markers.
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Best Local Similarity
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                                                                                                                                               (YEDA ) YEDA RES
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                        Unidentified
                                                                                                 24-SEP-1999;
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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides from the present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer accetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or mithody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chonic immune thyroiditis, autoimmune uveoretinitis, crohn's disease, chonic immune thyroiditis, autoimmune paramental purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, duillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriaats, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated'diseases which can be treated
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glatiramer acctate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipasoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatory arthritis; crohn; s disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
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                                                                                                                                                                                                                                                                                                       diabetes mellitus, Graves disease, Guillain-Barre's syndrome,
Hashimoto's disease, idiopathic myxoedema, myasthenia gravis;
pemphigus vulgaris; systemic lupus erythematosus.
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80.3%; Pred. No. 2.6e-13;
ive 2; Mismatches 1;
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Best Local Similarity
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weight TV-marker polypeptides (I) for determining the molecular weight of a copolymer (CE), which has an identified molecular weight of a copolymer (CE), which has an identified molecular weight of a copolymer (CE), which has an identified molecular weight of a copolymer (CE), which has an identified molecular weight can am amino acid composition corresponding to the copolymer. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibiody-mediated diseases. Such diseases include arthritic conditions, dampellinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic ansemis, autoimmune comportitis, autoimmune thyroiditis, autoimmune becomportitis, autoimmune thyroiditis, autoimmune aveoratinitis, contact sensitivity disease, dabetes mellitus, Graves purpura, collitis, contact sensitivity disease, dabetes mellitus, Graves disease, Gullian-Barre's syndrome, Hashimcto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-shot disease, and callayed-type hypersenaitivity. The polypeptides of the invention have defined molecular weights and phypatical properties which are analogous to molecular weight markers
                                                                                                                                                                                                                       glativamer acctate; autofamume disease; mattarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabethic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidiabethic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crow; disease; disease; disease; disease; disliain-Barre segura; colitis; diabetes mellitus; Graves disease; duillain-Barre segurace; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
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                                                                                                                                                          Copolymer molecular weight TV-marker amino acid sequence SEQ_ID NO:7.
                                                                                                                                                                                                         molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                             pemphigus vulgaris; systemic lupus erythematosus.
                       AAY82577 standard; peptide; 109 AA
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                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200018794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gad A, Lis D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-1999;
                                                                                                                28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2000.
                                                                   AAY82577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
AAY82577
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight cand an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune complete acetate diseases and inflammatory conditions, e.g. multiple antiple anthorisming diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune haemolytic conternitis, contact sensitivity disease, diabetes mellitus, Graves (Gesase, Guillain-Barre's syndrome, Hashimoto's disease, idopathic contact sensitivity disease, diabetes mellitus, or systemic confluence host-versus-graft disease, graft-versus-host disease, and cleaved confluence host-versus-graft disease, graft-versus-host disease, and delined molecular weights and physical properties of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                              glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyrominetic; haemostatic; antibaoriatic; dermatory; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guilain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                              Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                          AAY82572 standard; peptide; 45 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US22402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0101693.
                                                                                                                                                                                                                                                                                                          28-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200018794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lis D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-1998;
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                                                                                                                                                                                                                                                               AAY82572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gad A,
                                                                 40
                                                                                                                                                                         RESULT 6
AAY82572
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                                                                                                     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.9%; Score 180.5; DB 21; Length 109; 45.9%; Pred. No. 2.6e-11; ive 3; Mismatches 3; Indels 53;
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1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKAEAK------39

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AAR06446;
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                Sequence
                                       Query Match
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                                                                  Matches
                                                                                                                                                             RESULT 8
                                                                                                                                                                      AAR06446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for blosynthesis and blodegradation, especially blosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pot_sequences.
                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buchrieser C, Frangeul L, Couve E, Rusniok C, Faihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Varquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charif A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N, Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                              Gaps
                                                                                                                                                                                                                                                                                                      Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                       5, Indels 13;
                                                                                                       1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKY-KAEAAKAAAKEAAYEA
                                                 Score 134.5; DB 21; Length 45;
Pred. No. 4.7e-07;
0, Mismatches 5; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; SEQ ID No 1828; 192pp; French.
                                                                                                                                                                                                                                                                               Listeria monocytogenes protein #1827.
                                                                                                                                                                                               ABB49123 standard; Protein; 239 AA
                                                  50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2000; 2000FR-0004629
                                            Ouery Match
Best Local Similarity 68.4%
                                                                                                                                                                                                                                                  05-FEB-2002 (first entry)
 molecular weight markers
                                                                                                                                                                                                                                                                                                                                              Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-010914/01.
                          45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Voss H;
                                                                                                                                                                                                                                                                                                                                                                       WO200177335-A2
                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2001.
                                                                                                                                                                                                                         ABB49123;
                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rose M,
                                                                                                                                                                                 ABB49123
ID ABB
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                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also
                                                                                                                                                                                                                              1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAE-AKYKAEAAKAAAKEAAYE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids.
                                                                                                                            1;
                                                            DB 23; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.7%; Score 111; DB 11; Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing genes encoding random polymers of aminoacid(s) - i
producing recombinant polypeptide(s) with biological and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant copolymer 1-19, myelin basic protein analogue.
                                                                                                                         Indels
                                                         Score 116.5; DB 23;
Pred. No. 0.00018;
9; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                    AAR06446 standard; protein; 106 AA.
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                                                         43.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-1991 (first entry)
                                                                                          Local Similarity 55.4
nes 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunological activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-255848/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multiple sclerosis;
239 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-1989;
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular response to a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases. Such diseases include arthritic conditions, callerosis, rheumatoris and inflammatory conditions, e.g. multiple sclerosis, rheumatod arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chonic immune thrombocytopaenia purpura, colitis, context sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, didopathic myxoedema, myasthemia gravis, peomphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyvoid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Gulllain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                       Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.
                                   Gaps
                                                                                                   1 AKKYAKKEKAYAKKAEKAAKKAE------AKAYKAAEAKKKAEAKYKAEAAKA 47
                                 14;
Pred. No. 0.00027;
                              6; Mismatches
                                                                                                                                                                                                                                                                                                           AAY82571 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
        47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US22402,
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                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                              33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-317499/27
           Best Local Similarity
                                                                                                                                                            AAK-EAAYE 55
                                                                                                                                                                                    | | :|||:
AEKAKAAYK 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-SEP-1999;
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                              Matches
                                                                                                                                                          48
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The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA96456.198500 are used in the construction of the transporter system of the invention. The rucleic acids to hepatocytes, muscle cells or bone forming cells, e.g. for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transgenic animals (as models for treating cardiovascular disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in clude transforming cells to produce proteins, or transfecting cells in ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from endosomes, without requiring endosomal or lysosomal
                                                                                                                                                                                           3
delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                             26
                                                                                                                                                                                                                                                              35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
                                                                                                                                                                                                                                                   1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA
                                                                                                                                                          DB 21; Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #10 used in nucleic acid transporter system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WOO SLC,
                                                                                                                                                         39.3%; Score 104.5; DB 21;
51.8%; Pred. No. 0.00039;
tive 4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Column 125-128; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gottchalk S, Sparrow J, Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                    AAY98499 standard; Peptide; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-0167641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                           Local Similarity 51.8
Les 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-281993/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 AA;
                                                                                                                        35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6033884-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                     AAY98499;
                                                                                                                                                          Query Match
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                  AAY98499
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us-09-816-989a-3.open.rag

Matches

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AAY59044

Length 100;

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39.1%;
ilarity 58.2%;
Conservative
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nes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-365933/38
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6177554-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-1992;
19-MAR-1993;
 Query Match
Best Local Simi
Matches 32;
                                                                                                                                                                                                                                                    23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                     AAU04289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca]
Matches
                                                                                                                                                    RESULT 12
                                                                                                                                                                       AAU04289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a molety that recognizes and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through a nuclear membrane; and/or (e) a lysis moiety that enables the transport of the entire complex from the cells unface directly into the cytoplasm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to create transpont animals for a spessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells which allows the role of various nucleic acids to be studied by targeting specific expression into specifically targeted tissue culture cells. The lysis agent within the NTS avoids the problem of endosomal/lysosomal
                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
3..100
/note= "Lys-Ala in positions 3 to 100 may be optionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                                 Gaps
                                                                                                                                                                                                                                                                                                                   Nucleic acid transport system; NTS; cell surface receptor; cytosis; nuclear membrane; lysis moiety; transgenic animal; human disease;
                                                                  53
                                                                                ;
;
                                                                1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA
Score 104; DB 21; Length 100; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith LC;
                                 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sparrow J,
                                                                                                                                                                                                                                                                                    Amino acid polymer seq ID NO: 64 of US5994109.
                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Columns 123-124; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gottchalk S,
                                                                                                                                                                                AAY59044 standard; peptide; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             absent"
                                                                                                                                                                                                                                                                                                                                                      nucleic acid delivery; cancer
39.1%;
58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0167641.
92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0460890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0167641.
                                                                                                                                                                                                                                                    (first entry)
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-038262/03.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-1995;
                                                                                                                                                                                                                                                    07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-1993;
                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5994109-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                   AAY59044;
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100 AA;

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents poly-Lys-Ala, used to bind nucleic acid in a nucleic acid transporter system. The nucleic acid transporter system when the nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spacer molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Lys-Ala in positions 3-100 may be present absent"
                                                                                                                    53
                                                                                                                                                       1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                    1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sparrow J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.1%; Score 104; DB 22; Length 100; 58.2%; Pred. No. 0.0013; ive 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid transport; cytosis; ligand; lysis agent; gene therapy; hepatocyte; muscle; bone forming cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poly-Lys-Ala used in nucleic acid transporter system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gottchalk S,
Score 104; DB 21
Pred. No. 0.0013;
                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 131; 111pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith LC, Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                  AAU04289 standard; Peptide; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BAYU ) BAYLOR COLLEGE MEDICINE.
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92US-0855389.
93WO-US02725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a suchece ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can system can be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, apolloporteins, receptors, drugs, oncogenes, tumor antigens, tumor
                                                                                                                          Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel system (I) for delivering a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             suppressors, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                   Nucleic acid transporter system peptide ligand SEQ ID NO 64.
                                                                                                                                                                                                                                                                                                                                                                             WOO SLC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.1%; Score 104; DB 22; Length 100;
58.2%; Pred. No. 0.0013;
tive 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                           Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 125-126; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                           Gottchalk S, Sparrow J, Cristiano RJ,
                        AAB45852 standard; Protein; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR06445 standard; protein; 154 AA.
                                                                                                                                                                                                                                                                                                                                                  (BAYU ) BAYLOR COLLEGE MEDICINE,
                                                                                                                                                                                                                                                                                             93US-0167641.
92US-0855389.
                                                                                                                                                                                                                                                                       95US-0460971
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                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 58.2
1es 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-049093/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 AA;
                                                                                                                                                                 bacterial antigen
                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                             14-DEC-1993;
20-MAR-1992;
                                                                                                                                                                                                                                                                       05-JUN-1995;
                                                                         21-MAR-2001
                                                                                                                                                                                                                    US6150168-A.
                                                                                                                                                                                                                                                                                                                        19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-1991
                                                                                                                                                                                                                                             21-NOV-2000
                                                 AAB45852;
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RESULT 13
             AAB45852
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To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US(4691009, NREL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences.

A methionine residue occurs between the Protein A and rCOP-1 sequences. The cop-1 polypeptide may be cleaved from the fusion protein. rCOP-1-77 contains oligonucleotide duplexes incoding the following sequences: VKK, BEE, KAK, AAK, and AAA. The N-terminal alanine residue is left behind following CC receptalomyelitis. They are used to prevent, arrest or control a encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 AEAAAEAEKAKYKKKAKEAEYKKKAKAAAAEAEYKKEAEEAEYKKYKKKAKKAKKAKKAKE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Indels 24; Gaps
                                                  Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing genes encoding random polymers of aminoacid(s) - f
producing recombinant polypeptide(s) with biological and/or
immunological activity
Recombinant copolymer 1-77, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKEKA-YAKKAEKAKKAEAKAYKAAEAKKKAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 103; DB 11
Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY14928 standard; protein; 223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 11; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.7%;
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                                                                                                                                                                                                                                                                                                                                       90EP-0301700
                                                                                                                                                                                                                                                                                                                                                                                               90US-0473845
                                                                                                                                                                                                                                                                                                                                                                                                                          89US-0312541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REPL-) REPLIGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-255848/34.
                                                                                                              multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         See also AAQ05665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ05664
                                                                                                                                                                                                                                                                                                                                          16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-1990;
                                                                                                                                                                                                                                                                                    22-AUG-1990.
                                                                                                                                                                                                                            EP383620-A
                                                                                                                                                                      Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY14928;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cook KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
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ID AAY1
XX
AC AAY1
XX
DT 25-C
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4.

Amino acid sequence of M. vaccae antigen GV-45.

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The invention provides heat-killed Mycobacterium vaccae, or recombinant

M. vaccae proteins. The M. vaccae proteins may be employed to activate

T cells and natural killer cells, to stimulate the production of

cytokines, to enhance the expression of co-stimulatory molecules on

dendritic cells and monocytes, and to enhance dendritic cell maturation

and function. The proteins can be expressed by standard recombinant

and function. The proteins can be expressed by standard recombinant

and function, madequences encoding the proteins can be used for the

treatment, prevention, and detection of disorders including infectious

treatment acid sequences and cancer. In particular, the compounds and

methods are used for treatment of diseases of the respiratory system,

such as mycobacterial infections, asthma, allergies, tuberculosis,

such as mycobacterial infections, asthma, allergies tuberculosis,

psoriasis, atopic dermatitis, eccame, allergic contact dermatitis,

alopecia areata, and skin cancers such as basal carcinoma, squamous cell
                                  Mycobacterium vaccae protein; antigen; T cell activation; cytokine; dendritic cell maturation; infectious disease; immune disorder; cancer; respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma; squamous cell carcinoma; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.7%; Score 103; DB 20; Length 223;
Best Local Similarity 55.0%; Pred. No. 0.0038;
Matches 33; Conservative 3; Mismatches 18; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tan P, Visser ES, Watson J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enhancing immune response to an antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENESIS RES & DEV CORP LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 239; 243pp; English.
                                                                                                                                                                                                                                                                                                                             98US-0205426.
97US-0996624.
97US-0997080.
97US-0997362.
                                                                                                                                                                                                                                                                                           98WO-NZ00189
                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0156181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prestidge RL, Skinner MA,
                                                                                                                                                                        Mycobacterium vaccae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-430163/36.
N-PSDB; AAZ11393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 AA;
                                                                                                                                                                                                                                                                                         23-DEC-1998;
                                                                                                                                                                                                              WO9932634-A2
                                                                                                                                                                                                                                                   01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                    23-DEC-1997
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11-JUN-1998
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1 AKKYAKKEKAYAKKAEKAAKKAEAK----AYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56 8 셤

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Search completed: March 10, 2003, 12:21:29 Job time : 30.1814 secs

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GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model
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March 10, 2003, 12:26:10 ; Search time 16.6582 Seconds (without alignments) 141.764 Million cell updates/sec Run on:

US-09-816-989A-3 266

Title: Perfect score:

1 AKKYAKKEKAYAKKAEKAAK.......BAKYKAEAAKAAAKEAAYEA Sequence:

56

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188354 seqs, 42170167 residues Searched:

188354 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

Published Applications AA:\*

1: \cgn2\_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:\*

2: \cgn2\_6/ptodata/1/pubpaa/PCT NEW PUB.pep:\*

3: \cgn2\_6/ptodata/1/pubpaa/PCT NEW PUB.pep:\*

4: \cgn2\_6/ptodata/1/pubpaa/USO6 NEW PUB.pep:\*

5: \cgn2\_6/ptodata/1/pubpaa/USO6 NEW PUB.pep:\*

6: \cgn2\_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:\*

7: \cgn2\_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:\*

8: \cgn2\_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:\*

9: \cgn2\_6/ptodata/1/pubpaa/USO9 NEW PUB.pep:\*

10: \cgn2\_6/ptodata/1/pubpaa/USO9 NEW PUB.pep:\*

11: \cgn2\_6/ptodata/1/pubpaa/USO9 NEW PUB.pep:\*

12: \cgn2\_6/ptodata/1/pubpaa/USO9 NEW PUB.pep:\*

13: \cgn2\_6/ptodata/1/pubpaa/USO0 NEW PUB.pep:\*

14: \cgn2\_6/ptodata/1/pubpaa/USO0 NEW PUB.pep:\*

14: \cgn2\_6/ptodata/1/pubpaa/USO0 NEW PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		de				
Result		Query				
No.	Score	Match	Match Length DB	60	QI	Description
1	266	100.0	26	10	US-09-816-989A-3	Sequence 3, Appli
7	245.5	92.3	77	10	US-09-816-989A-5	Sequence 5, Appli
e	233	87.6	86	10	US-09-816-989A-6	9
4	198	74.4	99	10	US-09-816-989A-4	4, 7
S	180.5	67.9	109	10	US-09-816-989A-7	7
9	134.5	50.6	45	10	US-09-816-989A-2	7
7	105.5	39.7	372	0	US-09-820-843A-8	Sequence 8, Appli
80	104.5	39.3	35	10	US-09-816-989A-1	
σ	103	38.7	223	φ	US-10-051-643-201	Sequence 201, App
10	96.5	36.3		σ	US-10-184-832-5	Sequence 5, Appli
11	89.5	33.6	356	σ	US-09-820-843A-27	Sequence 27, Appl
12	82.5	31.0		φ	US-09-820-843A-95	Sequence 95, Appl
13	82	30.8		Φ	US-09-882-774-1	Sequence 1, Appli
14	82	30.8		10	US-09-815-242-13765	Sequence 13765, A
15	81	30.5		10	US-09-815-242-10314	Sequence 10314, A
16	80.5	30.3	309	Φ	US-09-820-843A-24	Sequence 24, Appl
17	80.5	30.3		10	US-09-864-761-36182	Sequence 36182, A
18	79	29.7	582	10	US-09-919-497-100	Sequence 100, App
19	78	29.3	218	σ	US-09-999-724-48	Sequence 48, Appl

Sequence 5854, Ap	Sequence 5, Appli	Sequence 37061, A	Sequence 90, Appl	Sequence 7, Appli	Sequence 5197, Ap	Sequence 9, Appli	Sequence 46, Appl	Sequence 11, Appl		Sequence 8, Appli	Sequence 35829, A	Sequence 35241, A	Sequence 3, Appli	Sequence 127, App	Sequence 1164, Ap	Sequence 128, App	Sequence 129, App	Seguence 130, App	Sequence 131, App	233,	Sequence 4122, Ap	Sequence 53, Appl	Sequence 51, Appl	Sequence 5198, Ap	Sequence 242, App
US-09-738-626-5854	9 US-10-093-892-5	10 US-09-864-761-37061	9 US-09-999-724-90	9 US-10-093-892-7	9 US-09-738-626-5197	9 US-10-093-892-9	9 US-09-999-724-46	10 US-09-893-238-11	9 US-09-985-442-8	10 US-09-983-580-8	10 US-09-864-761-35829	10 US-09-864-761-35241	10 US-09-124-280A-3	10 US-09-771-161A-127	10 US-09-925-300-1164	9 US-09-805-301-128	9 US-09-805-301-129	9 US-09-805-301-130	9 US-09-805-301-131	10 US-09-764-846-233	9 US-09-738-626-4122	10 US-09-883-825-53	10 US-09-883-825-51	10 US-09-815-242-5198	10 US-09-764-846-242
365	105	71	102	96	009	96	118	351	84	84	88	68	434	243	300	40	41	42	43	23	276	564	634	840	73
78 29.3	77.5 29.1	77 28.9	77 28.9	76.5 28.8	76 28.6	75.5 28.4	75 28.2	75 28.2	74 27.8	74 27.8	74 27.8	74 27.8	74 27.8	73 27.4	72.5 27.3	72 27.1	72 27.1	72 27.1	72 27.1		71.5 26.9			71.5 26.9	71 26.7
20	21	22	23		25		27	28	29	30	31	32	33	34		36	37	38	39			42			4.5

## ALIGNMENTS

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Sequence 3, Application US/09816989A

Sequence 3, Application US/09816989A

Sequence 3, Application US/09816989A

Sequence 3, Application US/09816989A

SEQUENCE 4, Application

SEQUENCE 5, DOIS

TITLE OF INVENTION: COPINER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI

TITLE OF INVENTION: COPOLYMER: 18/09/816,989A

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT PILING DATE: 1998-09-25

PRIOR FILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 3

LENGTH: 56

LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAEAKKKAEAKYKAEAAKAAAKEAYEA 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 266; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.8e-20;
Matches 56; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
US-09-816-989A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-816-989A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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Sequence 5, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: GAL Alexander
APPLICANT: Lis, Doris US-09-816-989A-5

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APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
FILE OF INVENTION: COPOLYMER I REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR PILING DATE: 1999-09-24
NUMBER OF SED ID NOS: 7
SOFTWARE: PATENTIN Version 3.1
SED ID NO 6
I.FNCTH. 84
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REPERENCE: 2609/60807-AP-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 00/101,693 PRIOR FILING DATE: 1998-09-25 PRIOR FILING DATE: 1998-09-24 SPRIOR FILING DATE: 1999-09-24 SP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----- 3EAK 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 92.3%; Score 245.5; DB 10; Length 77; Best Local Similarity 72.7%; Pred. No. 5.3e-18; Matches 56; Conservative 0; Mismatches 0; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 86;
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1. Similarity 62.8%; Pred. No. 9.9e-17;
54; Conservative 2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09816989A Patent No. US20020115103A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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Best Local Similarity
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US-09-816-989A-4
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; Sequence 4, Application US/0981698A
; Patent No. US20020115103A1
; GENERAL INFORMATION:
APPLICANT: Gad, Alexander
; APPLICANT: Gad, Alexander
; TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; SOFTWARE: PatentIn version 3.1
; SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKEKAY--AKKAE-KAAK--KAEAKAY-KAAEAKKK----AEAKYKAEAAKAAAK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 1.7e-11;
3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 198; DB 10
Pred. No. 2e-13;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEP'
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEP'
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR FILING DATE: 1998-09-25
PRIOR RILING DATE: 1998-09-25
PRIOR RILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.3%;
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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Best Local Similarity 45.9%;
Matches 50; Conservative
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: 02/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1999-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR PLING DATE: 1999-09-34
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 201, Application US/10051643

Sequence 201, Application US/10051643

Publication No. US20020197265A1

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L. J.

TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: System using Mycobacterium Vaccae

FILE REFERENCE: 11000.1008e2

CURRENT PAPLICATION NUMBER: US02.01-18

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1999-09-17

NUMBER OF SEQ ID NOS: 208

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 201

LENGTH: 223

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAYAKKAEKAAKKAEAK----AYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 104.5; DB 10;
Pred. No. 0.00015;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 38.7%; Score 103; DB 9;
1 Similarity 55.0%; Pred. No. 0.0014;
33; Conservative 3; Mismatches 18
Sequence 1, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.3%;
Best Local Similarity 51.8%;
Matches 29; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKA----AKKAYKK
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Best Local Similarity
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: ADD FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A.-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT PILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTING DATE: 1000-27
SEQ ID NOS: 7
SOFTWARE: PATENTING DATE: 1000-27
SEQ ID NOS: 7
SOFTWARE: PATENTING DATE: 1000-27
SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09820843A
Publication No. US20030039963A1
Publication No. US20030039963A1
GENERAL INFORMATION:
APPLICAT: Council of Scientific and Industrial Research
TITLE OF INVENTION: USFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USFUL AS ANTI-INFECTIVES
TITLE REPERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820, 843A
CURRENT FILING DATE: 2001-03-30
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 118
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 45;
     61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
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CTHER INFORMATION: outer membrane integrity protein (tolA)
NAME/KEY: misc_feature
CTHER INFORMATION: gi|1573353
US-09-820-843A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 134.5; DB 10;
Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                            ; Sequence 2, Application US/09816989A; Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 68.4%;
Matches 39; Conservative
                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gad, Alexander
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ORGANISM: H. influenzae
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US-09-816-989A-1
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                                                                                                                                                                                                                        Length 369;
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                                                                                                                                                                                                                                                                                                                             8 EKAYAKKAEKAAKK--AEAKAYKAAEAKKK-AEAKYKAEAAKAAAKEAAYEA
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APPLICANT: 2yskind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hodges, Robert

TITLE OF INVENTION: Use of Coiled-Coil Structural SC

TITLE OF INVENTION: Structure-Specific Peptides

FILE REFERENCE: 003592-007

CURRENT APPLICATION NUMBER: US/09/882,774

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,892

PRIOR PELICATION NUMBER: US 60/213,387

PRIOR FILING DATE: 2000-06-14
                                                      NAME/KEY: misc_feature;
CTHER INFORMATION: conserved hypothetical protein;
NAME/KEX: misc_feature
NAME/KEX: misc_feature
US-09-820-843A-95
                                                                                                                                                                                                                     Query Match 31.0%; Score 82.5; DB 9; Best Local Similarity 44.2%; Pred. No. 0.24; Matches 23; Conservative 11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
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Patent No. US20020061569A1
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PRIOR FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-882-774-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/09882774; Publication No. US20030021795A1; GENERAL INFORMATION: APPLICANT: Houston, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 16
        ORGANISM: T. pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-815-242-13765
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US-09-882-774-1
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Publication No. US20030039963A1
GRNERAL INFORMATION:
APPLICAMT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
TILE REPERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
SEQ ID NO 95
LENGTR: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/09820843A
Publication No. US20030039963A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
FILE REFERENCE: MPI2001-0656P1NM
CURRENT APPLICATION NUMBER: U3/10/184,832
CURRENT FILING DATE: 2002-06-28
PRIOR PILILGATION NUMBER: 60/303,250
PRIOR PILILGATION NUMBER: 60/303,250
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PASLEEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 452
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                                                                                                                                                                                                                                                                                                                                                                                                          36.3%; Score 96.5; DB 9; Length 452; 55.1%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 89.5; DB 9; Length 3.
Pred. No. 0.047;
6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
CTHER INFORMATION: tolA protein
NAME/KEY: misc_feature
OTHER INFORMATION: gi|9656364
US-09-820-843A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 33.6%;
Best Local Similarity 48.1%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 55.1
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Vibrio cholerae
                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mus musculus
US-10-184-832-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-820-843A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-820-843A-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 AERLAABEGAQREABEGARREABEGAKREAQQKAEREAAEQAKREAAEKAKREAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEA--KYKAEAAKAAAKEAA 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haselbeck, kobell
APPLICANT: Oblsen, Kari L.
APPLICANT: 29kind, Judith W.
APPLICANT: 29kind, Judith W.
APPLICANT: 28kind, Judith W.
APPLICANT: Amamoto, Nobert T.
APPLICANT: Carr, Grant J.
APPLICANT: Trawick, John D.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: Identification of Essential Genes in TILE OF INVENTION: Prokaryotes
FILE REPERENCE: BLITAL 0.11A
FILE REPERENCE: BLITAL 0.11A
CURRENT APPLICATION NUMBER: 06/191,078
FRIOR APPLICATION NUMBER: 60/191,078
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR PILING DATE: 2000-05-28
FRIOR PLING DATE: 2000-05-26
FRIOR PLING DATE: 2000-05-26
FRIOR PLING DATE: 2000-11-27
FRIOR PLING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/265,625
FRIOR PLING DATE: 2000-11-27
FRIOR FILING DATE: 2000-10-22
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-22
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-22
FRIOR FILING DATE: 2000-10-23
FRIOR FIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.5%; Score 81; DB 10; Length 890; 33.3%; Pred. No. 0.82; tive 17; Mismatches 13; Indels
FRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-12-22

PRIOR PELING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13765

TYPE: PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
CATTON: (1)...(892)
CATTON: (1)...(892)
US-09-815-242-13765
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.5
Best Local Similarity 33.3
Matches 21; Conservative
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6 KKEKAYAKK-----AEKAAKKAEAKAYKAAE--AKKKAEAKYKAEAAKEAA 53
                                                                                                                                                                       Search completed: March 10, 2003, 12:53:43
Job time : 17.8011 secs
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146 EQA 148
                                                                          54 YEA 56
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Sequence Sequence S Sequence

Sequence 2, Sequence 2, Sequence 2, Sequence 3, Sequence 2, Sequen

Perfect score:

Run on:

Scoring table: Sequence:

Database

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DB 4; Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER RELADED FORD ALSO MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A FILING DATE: 18-DEC-1997
PROGRAPPLICATION DATA: ROOM STATEMENT OF THE PROGRAPH OF THE 
                                                                                                                                    US-08-468-718-4

US-08-457-491A-5

US-08-214-164-2

US-08-214-164-2

US-08-247-852A-3

US-08-246-636-2

US-08-247-491A-3
                                                                                           US-08-214-222-4
US-08-467-852A-5
                                                                                                                                                                                                                                                                                                                                                  -08-312-949-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Greenlee, Winner and Sullivan STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder
                                                                                                                                                                                                                                                                                                      -08-319-795-2
                                                                                                                                                                                                                                                                                                                                                                                                  JS-08-469-434-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polycationic Oligomers
                                                                                                                                                                                                                                                                                                                              -08-468-985-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08993008A
Patent No. 6153596
GENERAL INFORMATION:
APPLICANT: Liotta, Dennis C.
APPLICANT: Petros, John A.
APPLICANT: Petros, John A.
APPLICANT: Rer, Joan F.
APPLICANT: Rey, Shiow-Jyi
APPLICANT: Pohl, Jan
TITLE OF INVENTION: Polycationic Ol
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION
TELEPHONE: 303-499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
    288
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; ANTI-SENSE: NO
US-08-993-008A-6
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COUNTRY: US
ZIP: 80303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-08-993-008A-6
  Query Match
  Sequence 64, Appl
Sequence 201, Appl
Sequence 201, Appl
Sequence 5, Appli
Sequence 27, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 2, Appli
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                                                                                                                                                        March 10, 2003, 12:15:04 ; Search time 9.92405 Seconds (without alignments) 166.029 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                    US-09-816-989A-3
266
1 AKKYAKKEKAYAKKAEKAAK......BAKYKABAAKAAAKEAAYEA 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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Sequence 6
Sequence 6
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Sequence 2
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued Patents AA:*

. /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
. /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
. /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
. /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
. /cgn2_6/ptodata/2/iaa/PcTuS_COMB.pep:*
                        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-993-008A-6
US-08-460-991A-64
US-08-460-911A-64
US-08-462-040-64
US-09-95-855-201
US-09-95-855-201
US-09-92-329-5
US-08-929-329-5
US-08-929-329-5
US-08-929-329-5
US-08-929-329-8
US-08-948-9-16
US-08-115-746-8
US-08-115-746-10
US-08-216-894-16
US-08-216-894-16
US-08-216-894-10
US-08-216-894-10
US-08-216-894-10
US-08-216-894-10
US-08-216-894-10
US-08-216-894-2
US-09-115-746-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-303-025-16
US-08-436-703B-4
                                                                                                                                                                                                                                                                                                                                                                                                                     262574 segs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .Query
Match Length
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103 101 99.5 94.5

Result No.

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 39.1%; Score 104; DB 3; Length 100; Best Local Similarity 58.2%; Pred. No. 0.0004; Matches 32; Conservative 4; Mismatches 17; Indels
                                                                                                                   GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gritchalk, Stephen
TITLE OF INVENTION: MUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Lys Ala" in positions 3 to 100 may present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FEASEM CON Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIPICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                      Sequence 64, Application US/08167641C
Patent No. 6033884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 64, Application US/08460971A
Patent No. 6150168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 205/0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELERX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Woo, Savio L.C.
Smith, Louis C.
Cristiano, Richard J.
                                                                                                                                                                                                                                                                                                                             AUDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
COTHER INFORMATION:
US-08-167-641C-64
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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APPLICANT: Woo, Sa
APPLICANT: Smith,
APPLICANT: Cristia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                    US-08-167-641C-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-460-971A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                              Gaps
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                              5;
                                                                                                    1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 39.1%; Score 104; DB 2; Length 100; Best Local Similarity 58.2%; Pred. No. 0.0004; Matches 32; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Getchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
Best Local Similarity 58.2%; Pred. No. 0.00022; Matches 32; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: 18M Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 20, 1993
APPLICATION NUMBER: 20, 1993
APPLICATION NUMBER: 20, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/066
                                                                                                                                                                                                                                      Sequence 64, Application US/08460890A
Patent No. 5994109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (213) 489-1600
(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
TELEFAX: (
                                                                                                                                                                                           RESULT 2
US-08-460-890A-64
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Sequence 201, Application US/09095855

Patent No. 6160093

GENERAL INFORMATION:

APPLICANT: Tan. Paul

APPLICANT: Skinner, Margot

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Compounds and Methods for

TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections

NUMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAKEAA 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.1%; Score 104; DB 4; Length 100; 58.2%; Pred. No. 0.0004; tive 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                    MEDIUM TYPE: storage
COMPUTER: INA Compatible
OPERATING TOWN IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFTCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 10, 1993
APPLICATION NUMBER: 07/859,389
FILING DATE: March 19, 1993
APPLICATION NUMBER: 20, 1992
APPLICATION NUMBER: 21,1993
APPLICATION NUMBER: 21,093
APPLICATION NUMBER: 32,327
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
FILENGOMMNICATION INFORMATION:
TELEPONE: (213) 489-1600
TELEFAX: (213) 555-0440
TELEFAX: (213) 555-0440
TELEFAX: (213) 555-0440
TELEFAX: (213) 550 10 NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                       COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.23
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98121
COMPUTER READABLE FORM
MEDIUM TYPE: Disket
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-09-095-855-201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 64, Application US/08462040

Patent No. 6177554

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gritiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-460-971A-64
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39.1%; Score 104; DB 4; Length 100;
Best Local Similarity 58.2%; Pred. No. 0.0004;
Matches 32; Conservative 4; Mismatches 17; Indels
                 TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS: 65
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                   COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1.5" DATA: 1.995
CLASSIFICATION NUMBER: 1.8/08/460,971A
PILING DATE: 1.995
FILING DATE: March 10, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 10, 1993
APPLICATION NUMBER: 10,1993
APPLICATION NUMBER: 20,1992
APPLICATION NUMBER: 20,1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
RELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
MEDIUM TYPE: 2001
                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Gottchalk, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-08-462-040-64
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1 AKKYAKKEKAY--AKKAE-----KAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAK
                                                                                                                             Sequence 5, Application US/08929329
Patent No. 6120770
GENERAL INFORMATION:
APPLICANT: APPLICANT: Dalton, John P
APPLICANT: APPLICANT: APPLICANT: Targpe, Stefan
TITLE OF INVENTION: Plasmodium Proteins Useful for Preparing
TITLE OF INVENTION: Vaccine Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/929,329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 101; DB 3;
Pred. No. 0.013;
4; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Greenlee, Winner and Sullivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polycationic Oligomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08993008A Patent No. 6153596
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Barnes & Thornburg
STREET: 11 S Meridian
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P
REGIGSTRATION NUMBER: 38,833
REFRENCE/DOCKET NUMBER: 9359:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-745
TELEPRAX: (317) 231-745
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1507 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Plasmodium yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 38.0%;
il Similarity 51.7%;
30; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liotta, Dennis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Petros, John A. APPLICANT: Wey, Shiow-Jyi APPLICANT: Karr, Joan F. APPLICANT: Pohl, Jan TITLE OF INVENTION: Polycat NUMBER OF SEQUENCES: GCORRESPONDENCE ADDRESS: ADDRESSE: Greenlee, Winn
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-08-993-008A-5
                                                                                                       US-08-929-329-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-929-329-5
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     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKEKAYAKKAEKAAKKAEAK---AYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFOGRATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Compounds of Mycobacterial Infections
FILE REFERENCE: 11000.1002.4
CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-10-4
EARLIER PLIING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER PLIING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: 08/873,970
EARLIER FILING DATE: 1997-06-12
EARLIER PLING DATE: 1997-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 103; DB 4; Length 223;
Pred. No. 0.0011;
3; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.7%; Score 103; DB 4; Length 223; Best Local Similarity 55.0%; Pred. No. 0.0011; Matches 33; Conservative 3; Mismatches 18; Indels
                           SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-ANG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-205-426-201
; Sequence 201, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 201: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Mycobacterium vaccae US-09-205-426-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.0%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
OPERATING SYSTEM:
                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-095-855-201
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LENGTH: 223
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Gaps
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APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Tood
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 35.5%; Score 94.5; DB 3; Length 214; Best Local Similarity 63.5%; Pred. No. 0.0078; Matches 33; Conservative 2; Mismatches 12; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.3%; Score 94; DB 1; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two Militia Drive
CITY: Lexington
STATE: Measachusetts
CITY: Lexington
STATE: Measachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTI Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cahryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTREISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-346-849-2
; Sequence 2, Application US/08346849
: Patent No. 5670483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brook, David E. REGISTRATION NUMBER: 22, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                     214 amino acids
                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-09-041-889-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5670483
GENERAL INFORMATION:
                                                                                                                                                                                                                                                     LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-346-849-2
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Fadence 27, Application US/09041889

Fatent No. 6033864

GENERAL INFORMATION:

APPLICANT: Braun, Jonathan

APPLICANT: Cohavy, Offer

TITLE OF INVENTION: Diagnosis, Prevention and Treatment of

TITLE OF INVENTION: Microbial UC pANCA antigens

TITLE OF INVENTION: Microbial UC pANCA antigens

NUMBER: OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.4%; Score 99.5; DB 4; Length 48; 58.3%; Pred. No. 0.00052; tive 4; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 KEKAYAKKAEKAAKKAEAKAYKAABAKKKAEAKYKAEA-AKAAAKEAA 53
                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FLING DATE: 18-DEC-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INPORMATION:
NAME: SUllivan, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/POCKET NUMBER: 33.95
TELEPHONE: 303-499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
  5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.3
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: 303-499-8089
INFORMATION FOR SEQ ID NO:
                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                           Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: not
MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE: NO
US-08-993-008A-5
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TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (<v. TELEFAX: (<v. TELEFAX: 04136
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 643 amino acide "vpE: amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                             CITY: Washington, D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-216-894-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            561 A 561
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                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: Rich, Alexander
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockehin, Cuttis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SBLF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                2 KKYAKKEKAYAKKAEKAAKK--AEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56
                                                                                                                2 KKYAKKEKAYAKKAEKAAKK--AEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA
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Patent No. 5876734
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.3%; Score 94; DB 2; Length 433; Best Local Similarity 47.4%; Pred. No. 0.018; Matches 27; Conservative 7; Mismatches 21; Indels
Best Local Similarity 47.4%; Pred. No. 0.018;
Matches 27; Conservative 7; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284A
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brook, David E. REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-600BA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08293284A
Patent No. 5955343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 433 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-293-284A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lexington
                                                                                                                                                                                                                                                                                                     RESULT 12
US-08-293-284A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-216-894-8
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYK-----AEAAKAAAKEA 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIAGNOSING INFECTION CRUZI
                                                                                                 COUNTRY: USA

ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION UNMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUPPLICATION NUMBER: US/09/115,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09115746
; Batent No. 6228601
; GENERAL INFORMATION:
; APPLICANT: Kirchhoff, Louis V.
; APPLICANT: Otsu, Keiko
; TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CUTY: Washington, D.C.
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
Elardner
STREET: 3000 K Street, N.W., Suite 500
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us-09-816-989a-3.open.rai

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WHEN ENTY Staphen A, REGISTRATION NUMBER, 19,778
REGISTRATION NUMBER, 19,786
TELERONA (202) 672-5399
TELERONA (202) 672-6399
T
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1;

Gaps

1;

Search completed: March 10, 2003, 12:30:02 Job time : 9.92405 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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protein search, using sw model OM protein Run on:

March 10, 2003, 12:15:04; Search time 19.3544 Seconds (without alignments) 327.825 Million cell updates/sec

US-09-816-989A-4

Perfect score:

313 1 AKKYAKKEKAYAKAKKAEAK......BAKYKABAAKAAAKEAAYBA 66 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

283224

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	membrane spanning	membrane spanning	tolA protein - Esc	histone H1, gonada	tolA protein [impo	sperm tail-specifi	Tola protein PA097	histone H1 - Chlam	outer membrane int	TolA colicin impor	histone H1 - sea u	mst101-1 protein -	histone Hī (clone	histone H1-gamma,	hypothetical prote	hypothetical prote	histone H1 - sea u	H1.10	histone H1A - Afri	outer membrane pro	probable erythrocy	probable hups - My	histone H1-beta, e	hypothetical prote	histone H1 homolog	zuotin - yeast (Sa	hypothetical prote	whe	R27-2 protein - Tr
SUMMARIES	ID	F90725	G85576	JV0057	HSUR1P	AG0592	S51364	E83525	829589	G64064	AC0138	806388	S34153	T06241	A26721	AE1689	AE1317	A25550	A28456	HSXL1A	B43592	T09127	G70673	A28100	T17698	861926	S25194	T06636	S22322	T30296
	98	~	7	~	-	~	~	~	7	~	7	7	7	ď	~	N	~	0	N	Н	N	~	7	7	7	7	~	0	~	~
	Query Match Length	394	394	421	248	376	1390	347	231	372	388	206	344	284	217	243	239	210	220	209	384	1701	214	211	311	182	433	924	236	1128
di	Query Match	42.3	42.3	41.9	39.3	39.1	38.8	38.2	37.7	37.5	37.4	36.9	36.7	36.1	35.9	35.8	35.6	35.5	35.1	34.8	34.2			33.5	•	32.9	32.7	32.6	32.4	32.4
	Score	132.5	132.5	131	123	122.5	121.5	119.5	118	117.5	117	115.5	115	113	112.5	112	111.5	111	110	109	107	107	106	105	104	103	102.5	102	101.5	101.5
	Result No.	1	7	٣	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19		21	22	23	24	25	56		28	29

histone H1 - rainb translation initia	histone HIA - Afri	histone H1.11L - c	conserved hypothet	histone H1 - musco	histone H1-II - Vo	cytosolic repetiti	histone H1 (clone	tolA protein VC183	arylesterase-relat	histone H1.03 - ch	histone H1 - trout	histone H1B - Afri	histone H1B - Afri	histone H1.C - Afr
HSTRIR E64114	151227	B28456	E75383	801262	JN0748	A44993	T06257	A82152	G87675	D28456	HSTR1	HSXL1B	151447	833219
7	~	0	N	~	~	N	N	N	N	N	Н	Н	N	~
206	229	225	581	218	241	328	288	356	438	224	194	219	220	221
							_	٠.		_		~	80	<b>&amp;</b>
32.3	31.8	31.6	31.6	31.5	31.5	31.5	31.3	31.2	31.2	31.0	30.8	30.8	30.	30.
	99.5 31.8													

## ALIGNMENTS

A;Status: preliminary
A;Atatus: Lyge: DNA
A;Molecule type: DNA
A;Residues: 1.734 «HAY»
A;Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC80774

9. Length 394; Query Match
42.3%; Score 132.5; DB 2; Length
Best Local Similarity 58.9%; Pred. No. 0.00099;
Matches 43; Conservative 8; Mismatches .13; Indels

4

1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAA-----KAEKKEYAAAEAKYKAEA 54 ð

g

55 AKAAA-KEAAYEA 66 ò

|||| |:|| :| 214 EKAAADKKAAEKA 226 d

RESULT 2

G85576

membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain 1

C;Bocies; Escherichia coli
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Nov-2001
C;Accession: G8576
R;Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-394 <STOA;Cross-references: GB:BE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:GN00145; UWGP:209
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:

A, Gene: tolA

2,

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A,Reference number: A201096, MUID:80156831; PMID:6767609
A,Rocession: A31090
A,Rocession: A31090
A,Rocession: A31090
A,Rocession: A31090
A,Rocession: A31090
A,Rocession: A31090
A,Rocession: A31091
B,Strickland, W.N.; Strickland, M.; Brandt, W.F.; von Holt, C.; Lehmann, A.; Wittmann-Li
R,Strickland, W.N.; Strickland, M.; Brandt, W.F.; von Holt, C.; Lehmann, A.; Wittmann-Li
R,Strickland, W.N.; Strickland, M.; WID:80156832; PMID:7363905
A,Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus angu-
A,Reference number: A31091; MUID:80156832; PMID:7363905
A,Reference number: A31091
A,Residues: 80-248 <ST2>
A,Rolecule type: protein
A,Residues: 80-248 <ST2>
A,Note: 144-Arg was also found
C,Superfamily: histone H1
C;Superfamily: histone H1
C;Keywords: DNA binding; nucleosome; sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tollA protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) C;Species: Salmonella enterica subsp. enterica serovar Typhi (c;Species: Salmonella enterica subsp. enterica serovar Typhi (c;Species: Date: Da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S51364
sperm tail-specific protein mstl01(2) - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S51364; S34154
R;Neesen, J.; Padmanabhan, S.; Buenemann, H.
Eur. J. Blochem. 225, 1089-1095, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 АКККАБАБААКАААБЕКККАБАБААКААДАКККАДДЕЛАКАДАБАКККАДДААК---- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KYAKKEKAYAKAKKAEAKAAKKA-KAEAKKYAKAAKAEKKEYAA-AEAKYKAEAAKAAAK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 248;
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Pred. No. 0.0058;
4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 39.3%; Score 123; DB 1; Similarity 56.1%; Pred. No. 0.0039; 37; Conservative 7; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.1%;
51.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 EAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
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C(3) Species Escherichia coll
E(4) Species Escherichia coll
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E(5) Species Escherichia
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Histone H1, gonadal - sea urchin (Parechinus angulosus)

C;Species: Parechinus angulosus (angulate urchin)

C;Date: 31-Mar-1980 #sequence_revision 31-Mar-1980 #text_change 16-Feb-1997

C;Accesabion: A91090; A91091, A02586

R;Strickland, W.N.; Strickland, M.; de Groot, P.C.; von Holt, C.; Wittmann-Liebold, B.

Eur. J. Biochem. 104, 559-566, 1980

A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus ang
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                                                                                                                                                                       1 AKKYAKKEKAYAKAKAEAKAAKKAKAEAKKYAKAA-----KAEKKEYAAAEAKYKAEA 54
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                    Length 394;
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            Score 132.5; DB 2;
Pred. No. 0.00099;
8; Mismatches 13;
                42.3%;
58.9%;
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                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        214 EKAAADKKAAEKA 226
                                                                                                                                                                                                                                                                                                                              55 AKAAA-KEAAYEA 66
                                                 Local Similarity
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                                                                                     43;
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            Query Match
Best Local Si
Matches 43;
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1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKA-----AKAEKKEYAAAEAKYKAE 53
                                                                                                                         A,Molecule type: DNA
A,Residues: 1-231 <FAB>
A,Cross-references: EMBL:U16726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JC5212
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KSA 221
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A,Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represe lpha-helical rods within the extremely elongated spermatozoa of Drosophila hydei. A,Reference number: S51364; MUID:95045538; PMID:7957199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TolA protein PA0971 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Dseudomonas aeruginosa
C;Species: Dseudomonas aeruginosa
C;Accession: E83525
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
R;Stover, C.K.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Accession: E83525
A;Accession: E83525
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
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C;Date: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 23-Jul-1999
C;Accession: S59589; S62122
R;Fabry, S.; Mueller, K.; Lindauer, A.; Park, P.B.; Cornelius, T.; Schmitt, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAK---KEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKA 57
                                                                     A; Accession: S51364
A; Status: nucleic acid sequence not shown
A; Status: nucleic acid sequence not shown
A; Status: nucleic acid sequence not shown
A; Residues: 1-1390 «NEE>
A; Cross-references: EMEL:X73481
R; Neesen, J: Heinlein, U.A.O.; Buenemann, H.
Submitted to the EMEL Data Library, June 1993
A; Reference number: S34153
A; Accession: S34154
A; Molecule type: DNA
A; Residues: 1-163, E'. 164-236, 'Q', 237-254, 257-320, 'E', 321-1390 «NEW>
A; Cross-references: EMEL:X73481; NID:g313201; PID:g313202
C; Genetics:
A; Gene: mst101(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

38.8%; Score 121.5; DB 2; Length
Best Local Similarity 59.7%; Pred. No. 0.019;
Matches 37; Conservative 3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: FlyBase: FBgn0011816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S59589
histone H1 - Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-347 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: tolA; PA0971
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A;Reference number: S59581; MUD:96120862; PMID:8590479
                                                                                                                                                                                                                                                                                                            A;Note: the authors did not translate the codon for residue 1
R;Fabry, S.; Ford, C.; Lindauer, A.; Mueller, K.; Cornelius, T.; Schmitt, R.
submitted to the EMBL Data Library, October 1994
A;Description: The organization, structure and controlling elements of Chlamydomonas hist A;Reference number: S62122
A;Accession: S62122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 'V',2-47,'A',49-141,'R',143-164,'P',166-189,'R',191-202,'A',204-226,'A',228-:
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C;Accession: G64064; UC5212

F; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, R.; Gocam, D.M.; Brandon, J.D.; Goct, U.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A)Residues: 1-372 <TIGR>
A)Residues: 1-372 <TIGR>
A)Cross-references: GB:U3272; GB:L42023; NID:g1573348; PIDN:AAC22041.1; PID:g1573353; R)Sen, K.; Sikkema, D.J.; Murphy, T.F.
Gene 178, 75-81, 1996
A)Title: Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Isolation and characterization of the Haemophilus influenzae tol0, tolR, A;Reference number: JC5212; MUID:97080550; PMID:8921895
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C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-173,'P',174-231 <FAW>
A;Cross-references: EMBL:U16726; NID:g571479; PIDN:AAA98452.1; PID:g571480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
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A;Note: the authors translated the codon CGT
                                                                                                                                                            A;Status: nucleic acid sequence not shown A;Molecule type: DNA
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histone H1 (clone TH315) - wheat
C;Species: Triticum aestivum (common wheat)
C;Species: Triticum aestivum (common wheat)
C;Accession: 10-Apr. 1999 #sequence_revision 30-Apr. 1999 #text_change 21-Jul-2000
C;Accession: T66241
R;Tacka, K.; Ohtsubo, N.; Fujimoto, Y.; Mikami, K.; Meshi, T.; Iwabuchi, M.
Plant Cell Physiol. 39, 294-306, 1998
A;Title: The modular structure and function of the wheat H1 promoter with S phase-specif,
A;Reference number: Z15562; MUID:98249625; PMID:9588026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A26721
histone H1-gamma, embryonic - sea urchin (Strongylocentrotus purpuratus)
c)species: Strongylocentrotus purpuratus (purple urchin)
c)species: Strongylocentrotus purpuratus (purple urchin)
c)bate: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C;Accession: A26721
R;Knowles, J.A.; Lai, Z.C.; Childs, G.J.
R;Knowles, J.A.; Lai, Z.C.; Childs, G.J.
A;Title: Isolation, characterization, and expression of the gene encoding the late histor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:D87064; NID:g2980890; PIDN:BAA25203.1; PID:g2980891
A;Experimental source: clone TH315
                             97 AKKEKEAAEKKKC-AEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKK 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 284;
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                                                                                                                                                                                                                                                                                                                    A, Cross-references: EMBL:X73480; NID:g313199; PID:g313200 C, Genetics:
A, Gene: FlyBase:Dhyd/mst101
A, Cross-references: FlyBase:PBgn0011816
C, Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AKKEKAYAKAKKAEAKAAKKAK--AEAKKYAKAAKAE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: T06241
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.021;
mst101-1 protein - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
C;Accesion: 334153
R;Neesen, J.; Heinlein, U.A.O.; Buenemann, H.
Bubmitted to the EMBL Data Library, June 1993
A;Reference number: S34153
A;Accession: S34153
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-344 <NEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.7%; Score 115; DB
49.4%; Pred. No. 0.02
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 KCAEAAKKEKEAAEKKKCAEA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 YKAEAAK----AAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 72/3
C; Superfamily: histone H1
C; Keywords: DNA binding; nucleus
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Best Local Similarity
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hes 32; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-284 <TAO>
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Matches
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                                                                                                                                                                                                                       RESULT 10
AC0138
Tolacidin import membrane protein [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AC0138
R;Parkhill, J; Wren, B.W; Thomson, N.R.; Titball, R.W; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.W.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 253-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Recession: AC0138
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 «KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89966.1; PID:g15979190; GSPDB:GN00175
C;Genetics:
A;Gene: tolA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
5.09388
histone H1 - sea urchin (Parechinus angulosus)
C;Species: Parechinus angulosus (angulate urchin)
C;Species: Parechinus angulosus (angulate urchin)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S09388
R;Hill, C.S.; Martin, S.R.; Thomas, J.O.
EMBO J. 8, 2591-2599, 1989
R;Hill, C.S.; Martin, S.R.; Thomas, J.O.
EMBO J. 8, 2591-2599, 1989
R;Hill, C.S.; Martin, S.R.; Thomas, J.O.
A;Attler: A stable alpha-helical element in the carboxy-terminal domain of free and chrom A;Reference number: S09388; MuID:90060019; PMID:2583125
A;Accession: S09388
A;Accession: S09388
A;Accession: S09388; MuID:90060019; PMID:2583125
C;Superfamily: histone H1
C;Keywords: chromosomal protein
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        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKYAKKEKAYAKAK----KAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---AEAK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.4%; Score 117; DB 2; Length 388;
49.3%; Pred. No. 0.016;
iive 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KYAKKEKAYAKAKKAEAK---AAKKAKAEAKKYAKAAKAEKKEYAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 KKKTÄÄKKÄKKPÄÄKKÄ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                il Similarity 49.39
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 YKAEAAKAAAKEAAYEA
                                                                                                                                                 228 AEAKAATEAKRKA 240
                                                                                             54 AAKAAAKEAAYEA 66
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Best Local Similarity
Matches 38; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || :||
219 KAAADAA 225
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Matches 3
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S34153
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A; Reference number: A26721; MUID:87172742; PMID:3031476

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A, Accession: A26721
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-217 <KNO>
A; Cross-references: GB:M16033; NID:g161517; PIDN:AAA30059.1; PID:g161518
C; Superfamily: histone H1
C; Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
F; 2-217/Product: histone H1-gamma, embryonic #status predicted <MAT>
                                                                                                                                                                                                                                           Query Match
35.9%; Score 112.5; DB 2; Length 217;
Best Local Similarity 49.4%; Pred. No. 0.023;
Matches 38; Conservative 3; Mismatches 21; Indels 15;
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RESULT 15
AE1689
hypothetical protein homolog lin2055 [imported] - Listeria innocua (strain Clip11262)
C; Species: Listeria innocua
C; Date: 27-Nov-2001
C; Species: Listeria innocua
C; Date: 27-Nov-2001
C; Accession: AE1689
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
J; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 224, 4849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A; Reference number: AB1077; MUD:21537279; PMID:11679669
A; Accession: AE1689
A; Status: preliminary
A; Moseidues: 1-243 cGLA>
A; Kesidues: 1-243 cGLA>
A; Kross-references: GB:AL592022; PIDN:CAC97285.1; PID:g16414556; GSPDB:GN00178

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A;Gene: lin2055

Query Match 35.8%; Score 112; DB 2; Length 243; Best Local Similarity 47.1%; Pred. No. 0.028; Matches 32; Conservative 11; Mismatches 23; Indels

1;

Gaps

5

1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAE--AKYKAEAAKAA 58 ઠ g

59 AKEAAYEA 66 ò

170 KEKAAAEA 177

Search completed: March 10, 2003, 12:28:27 Job time : 19.3544 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 10, 2003, 12:15:01 ; Search time 15.038 Seconds
 (without alignments)
 182.035 Million cell updates/sec Run on:

US-09-816-989A-4 313 1 AKKYAKKEKAYAKKKAEAK......BAKYKAEAAKAAAKEAAYEA 66 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P19934 escherichia P0226 parechinus Q08696 drosophila P50600 pseudomonas P44678 haemophilus Q08695 drosophila Q087796 strongyloce Q9zhc5 mycobacteri P06144 lytechinus Q9xb18 mycobacteri P06892 xenopus lae P27806 trittcum ae P27807 accharomyc Q93mh5 klebsiella P5087 saccharomyc Q93mh5 klebsiella P60850 oncorhynchu P40327 chironomus P44323 haemophilus P06350 oncorhynchu P60350 saccharomyc Q93mh5 klebsiella P60896 salop P08287 gallus gall P08264 salmo trutt P15866 xenopus lae P6254 salmo trutt P15866 xenopus lae P069987 gallus gall
SUMMARIES	TOLIA BCOLI H1 PĀRAN H872 DROHY TOLIA PERBE TOLIA PERBE TOLIA PERBE TOLIA PERBE TOLIA PERBE H1 LYPPI DBH WYCHO H1 LYPPI H1 LYPPI H1 STRPH H1 CHITE H1 CHITE H1 CHITE H1 CHITE H1 CHITE H1 OWCMY H1 LOWCMY H1 LOWCM
98	
% Query Match Length	1 2 4 1 1 2 4 1 1 1 2 4 2 1 1 1 2 4 2 1 1 1 2 4 2 1 1 2 4 2 1 1 2 4 2 1 1 2 1 2
% Query Match	4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
Score	11212331111111111111111111111111111111
Result No.	1 1 2 6 4 2 6 7 6 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7

P40277 chironomus P15867 xenopus lae P40275 chironomus P40278 chironomus P12036 homo sapien P08284 gallus g
HIC_CHITE HIGZ_XENLA HIA_CHITE HIA_CHITE NEH_HUMAN HIO_CHICK HII_CHICK HII_CLYSA HII_CLYSA HII_CLYSA HII_CLYSA HII_CLYSA
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221 220 237 237 237 218 233 225 233 218
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# ALIGNMENTS

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Strickland M., de Groot P.C., von Holt C.,
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InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; LinkerhIst_N.
Pfam; PF00538; Linker histone; I.
ProDom; PD000373; Linkerhist_N: 1.
                                                                       Cyanogen bromide peptides.";
Eur. J. Biochem. 104:559-566(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 56.1 tes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       144
Strickland W.N., Stri
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 KAAKKA 185
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Q08696;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAYAKAK-----KAEAKAAKKAKAEAKKYAK-----AAKAEKK-EYAAAEA 48
                                                                                                                                                                                                 OF BACTERIOPHAGE DNA. SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EcoGene; EG11007; tolA.
Transport; Protein transport; Bacteriocin transport; Transmembrane;
                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                PERIPLASMIC (POTENTIAL).
DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Indels 12;
              "TolA central domain interacts with Escherichia coli porins.";
EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 131; DB 1; Length 421;
Pred. No. 0.00058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Histone Hi, gonadal.
Parechinus angulosus (Angulate sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa;
Echinoidea, Euechinoidea, Echinacea, Echinoida, Echinidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat; Inner membrane; 3D-structure; Complete proteome. DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (2,4).
8B2F52B4B97C655E CRC64;
                                                        X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-84.
MEDLINE=80156831; PubMed=6767609;
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M28232; AAA24683.1; -. EMBL; AE000177; AAC73833.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 AA; 43156 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D90713; BAA35405.1; -. PIR; JV0057; JV0057. PDB; LTOL; 20-MAY-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.9%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 KKKAEAAEAAAAEAKKA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
421
421
421
278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35
48
                                                                                                                                                                                                                               AND LAMB
Lloubes R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parechinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H1_PARAN
P02256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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SEQUENCE OF 80-248.
MEDINE=80156832; PubMed=7363905;
Strickland W.N., Strickland M., Brandt W.F., von Holt C., Lehmann A.,
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 1. Chemical and enzymatic fragmentation of the protein and the sequence of amino acids in the four N-terminal
                                                                                                                                                                                                                                                                                                                                                                                   "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 2. Sequence of the C-terminal CNBr peptide and the entire primary structure.";

Eur. J. Biochem. 104:567-578 (1980)

-!- FUNCTION: HISTONES H1 ARB NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.

-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MST101(2).
Drosophila hydei (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KYAKKEKAYAKAKKAEAKAAKKA-KAEAKKYAKAAKAEKKEYAA-AEAKYKAEAAKAAAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95045538; PubMed=7957199;
Neesen J., Padmanabhan S., Buenemann H.;
Nandemly arranged repeats of a novel highly charged 16-amino-acid motifi representing the major component of the sperm-tail-specific axoneme-associated protein family Dhmst101 form extended alpha-helical rods within the extremely elongated spermatozoa of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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Eur. J. Biochem. 225:1089-1085(1994).

-i- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL.

-i- SUBCELLULAR LOCATION: Cytoplasmic.

-i- TISSUE SPECIFICITY: TESTIS. PRIMARY SPERMATOCYTES AND EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.3%; Score 123; DB 1; Length 24 56.1%; Pred. No. 0.0016; tive 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 AA; 26387 MW; 1B25B3F136541947 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- TISSUB SPECIFICITY: SPERM.
-i- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
PIR; A02586; HSURIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Axoneme-associated protein mst101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1391 AA.
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FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                             347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          Complete proteome.
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                                                                 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                           209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 AARKAA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 AAKEAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOLA OR HI0383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 34;
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TRANSMEM
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                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iBo-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ñ
                   DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELLCAL.
POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=LO43137; Pubmed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Weetbrook-Wadman S., Yuan Y., Brody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Raith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.",
                                                                                                                                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             656 KKLAKKEKETAEKKKCE-KAAKKRKEBAEK-KKCAEAAKKEKEAAEKKKCEEAAK-KEKE 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KKYAKKEKAYAKAKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKE 61
                                                                                                                                                                                                                                                                                                                                                         Sperm; Repeat; Multigene family; Polymorphism.

DOMAIN 332 1268 59 x 16 AA APPROXIMATE TANDEM REPEATS |
59 x 16 AA APPROXIMATE TANDEM REPEATS |
51 x 16 AA APPROXIMATE TANDEM REPEATS |
52 x 16 AA APPROXIMATE TANDEM REPEATS |
53 x 16 AA APPROXIMATE TANDEM REPEATS |
54 x 16 AA APPROXIMATE TANDEM REPEATS |
55 x 16 AA APPROXIMATE TANDEM REPEATS |
56 x 16 AA APPROXIMATE TANDEM REPEATS |
57 x 16 AA APPROXIMATE TANDEM REPEATS |
58 x 16 AA APPROXIMATE TANDEM REPEATS |
58 x 16 AA APPROXIMATE TANDEM REPEATS |
59 x 16 AA APPROXIMATE TANDEM REPEATS |
50 x 16 AA APPROXIMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dennis J.J., Lafontaine B.R., Sokol P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 121.5; DB 1; Length
Pred. No. 0.0086;
3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0020733; Dhyd\mst101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97113525; PubMed=8955385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.8%;
59.7%;
                                                                                                                                                                                                                                                                                              EMBL; X73481; CAA51876.1; -. PIR; S34154; S34154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 59.7
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOLA OR PA0971.
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SPERMATIDS
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                                                                                     REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=RG / KW20 / ATCC 51907;

MEDLINE=55350630; PubMed=7542800;

MEDLINE=55350630; PubMed=7542800;

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAK----KEKAYAKAKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAAEAKYKAEAAKA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fransport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97080550; PubMed=8921895;
Sen K., Sikkema D.J., Murphy T.F.;
Isolation and characterization of the Haemophilus influenzae tolQ,
tolR, tolA and tolB genes.";
Gene 178:75-81(1996).
(BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.2%; Score 119.5; DB 1; Length 347; 51.5%; Pred. No. 0.0039; tive 7; Mismatches 22; Indels 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEDD4B04AA095945 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P44678; P94810;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-ALA
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37 PO
347 PE
216 PO
37935 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE004530; AAG04360.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U39558; AAC44660.2; -.
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PIR; A26721; A26721
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H1G_STRPU
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                                                                                                                                                                                                                                                                                                                                            요
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                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neesen J., Buenemann H., Heinlein U.A.,
"The Drosophila hydei gene Dhmst101(1) encodes a testis-specific,
repetitive, axoneme-associated protein with differential abundance in
Dev. Biol. 162:414-425(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Perygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7224,
                                                                                                                                                                      Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
         (BY SIMILARITY).
SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKA-----AKAEKKEYAAAEAKYKAE
 FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                             7 ;
                                                                                                                                                                                                                                                                                 STRAIN 1479)
                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                            22; Indels
                                                                                                                                                                                                                                                                                                                      -> S (IN STRAIN 1479).
-> A (IN STRAIN 1479).
-> P (IN STRAIN 1479).
266ECF05C6C95544 CRC64;
                                                                                                                                                                                                                                                 A -> 8 (IN STRAIN 1479)

V -> A (IN STRAIN 1479)

D -> A (IN STRAIN 1479)

A -> ARAAABARAKA (IN STRAIN 1479)

T -> A (IN STRAIN 1479)

I -> V (IN STRAIN 1479)

N -> S (IN STRAIN 1479)
                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                            1479)
                                                                                                                                                                                                                       V -> A (IN STRAIN
K -> R (IN STRAIN
                                                                                                                                                                                                                                           (IN STRAIN
                                                                                                                                                                                                                                                                                                                                                                        37.5%; Score 117.5; DB : 46.6%; Pred. No. 0.0059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. 31, Last sequence update)
1. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches
                                                                                                                                                                                                              PERIPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                            333 S
39831 MW;
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                                                                                                                               EMBL; U32722; AAC22041.1; -. EMBL; U32470; AAC44596.1; -.
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Drosophila hydei (Fruit fly).
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223
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254
306
323
333
372 AA;
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                  Complete proteome
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                             (Potential)
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16-OCT-2001
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MST1_DROHY
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Knowles J.A., Lai Z.-C., Childs G.J.;
"Isolation, characterization, and expression of the gene encoding the
late histone subtype H1-gamma of the sea urchin Strongylocentrotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AKKEKAYAKAKKAEAKAAKKAK-AEAKKYAKAAKAE------KKEYAAAEAK 49
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                                                                                                                                                               -i- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
-i- POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN STRAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOLIA CELL. BIOL. 7:478-485 (1987).
-!- FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OVCIEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL. IT
                                  ASSOCIATED WITH AXONEMAL STRUCTURES.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
TISSUB SPECIFICITY: TESTIS. LOCATED IN SPERMATOCYTES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Indels
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Pred. No. 0.0087;
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01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1-gamma, late.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.7%; Sco...
49.4%; Pred. No. v...
... 4; Mismatches
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FlyBase; FBgn0011816; Dhyd\mst101(1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 YKAEAAK----AAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X73480; CAA51875.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M16033; AAA30059.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                SPERMATID BUNDLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
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Mol. Cell. E
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                                 111 AKKAAKKAPAKKAAAKKTATKAAAKKAPAKKAATKAPAKKAATKAPAKKAATKAPAKKA- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.5%; Score 111; DB 1; Length 210;
48.6%; Pred. No. 0.012;
tive 4; Mismatches 23; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 АКККЕОКЕККААКТКАВКЕКГААККААККААККҮККРАККРАККААККРААККАА-К 171
                                                                                                                                                                                                                                                                                                                                                           Lytechinus pictus (Painted sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
-----AKKAEAKA-AKKA--KAEAKKYAKAAKAEKKE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 210 AA; 21746 MW; 08C33F64894007E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKEKAYAK-----AKKAEAKAAKKAKAKAEAKKYAKAAKAEKKEYAAAEAKYK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                      210 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X04488, CAA28177.1; -. PTR, A25550. A2550. HSSP: P02259, 1HST. InterPro; IPR001386, Histone H1/H5. InterPro; IPR003216; Linkerhist N. Pfan, PP00338, linker histone; I. ProDom; PD000373, Linkerhist N. SMART; SM0526; Hi5; 1.
                                                                                                                           - AATKAPAKKAAAKAPAKKAATKA 191
                                                                                  43 YAAAEAKYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 48.6
Matches 35; Conservative
                                                                                                                                                                                                                                    STANDARD;
  1 AKKYAKK---EKAYAK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 KPAAKKPAKKAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 AEAAKAAAKEAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7653;
                                                                                                                                                                                                                                                                                                                                             Late histone H1
                                                                                                                                                                                                                                    H1 LYTPI
P06144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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DBH MYCBO
ID DBH M
AC Q9XB1
DT 16-OC
                                                                                                                             169
                                                                                                                                                                                                                H1_LYTPI
ID_ H1_I
                                                                                                                                                                                         RESULT 9
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                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                               1 AKKYAKKEK----AYAKAKAEAK-----AAKKAKAEAKKYAKAAK---AEKKEYAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
           InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; LinkerhIst N.
Pfam; PF00538; linker histone; I.
Probom; PD000373; Linkerhist N; I.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 217 AA; 22658 MW; C7251EED3413B185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOI. Genet. 260:475-479(1998).

-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBI_TaxID=1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 700084 / mc(2)155;
MEDLINE=99110209; Pubmed=9894918;
Lee B.H., Murugasu-Oei B., Dick T.;
"Upregulation of a histone-like protein in dormant Mycobacterium smegmatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                  3; Mismatches 21; Indels 15;
                                                                                                                                                                                         y Match 35.9%; Score 112.5; DB 1; Length 217; Local Similarity 49.4%; Pred. No. 0.0093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp).
HUP OR HLP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEGENERAL HISTONE-LIKE DOMAIN.
DEGENERATE REPEATS REGION.
CASP577F61F7EF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.6%; Score 111.5; DB 1; Length 2
50.0%; Pred. No. 0.011;
ive 5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding; DNA condensation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P02346; IHUU.
InterPro; IPR000119; Bac DNAbind.
Pram; PP00216; Bac DNA binding; 1.
ProDom; PD000945; Bac DNAbind; 1.
SMART; SM00411; BHL; 1.
PROSITE; PS00045; HISTONE_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF068138; AAD13809.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 AA; 21230 MW;
                                                                                                                                                                                                                                                                                                                                                                                          || |: || || |
199 KPAKKAAKPA 215
                                                                                                                                                                                                                                                                                                                                                                 46 AEAKYKAEAAKAAAKEA 62
                                                                                                                                                                                                                                    Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205
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                                                                                                                                                                                         Query Match
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RESULT 8 DBH\_MYCSM

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Best Local Matches 4

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  Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 KKAAAAKKSPKKAKKPAAATKKAAKSPKKATKAAKPKKAATAKSPAKAKAVKPKAAKPK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KKYAKKEKAYAKAAKAAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAKE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                 MEDIINE=87250632; PubMed=3597432;
Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;
Characterization of the chicken histone H1 gene complement.
Generation of a complete set of vertebrate H1 protein sequences.";
J. Biol. Chem. 262:9656-9663(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia; Batrachia; Anura, Mesobatrachia; Pipoidea, Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                  οŧ
                                                                                                                                                                                                                                                                               MEDLINE=98060905; PubMed=9396815; Schwarz S., Hess D., Jost J.P.; hrespirated DNA binding protein-2-H1 (MDBP-2-H1) consists of histone H1 subtypes which are truncated at the C-terminus."; Nucleic Acids Res. 25:5052-5056(1997).
-!-FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEGOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELJULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACETYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 GLOBULAR.
21872 MW; A944DF6C0D3048AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone HIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 AA.
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MEDLINE=86037224; PubMed=3863963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001386; Histone H1/H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00538; linker histone; 1. ProDom; PD000373; Linkerhist_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M17018; AAA48788.1; -.
                                                                                                                                                                                                                                                            IDENTIFICATION OF ALA-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00526; H15; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A28456; A28456.
HSSP; P08287; 1GHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 1
219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                              SEQUENCE FROM N.A.
                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8355;
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INIT MET
MOD RES
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Local 5.
30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H1A XENLA
P06892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4,
                                                                                                                                                                                                                                                                                                                                                                                                                    from Mycobacterium.",
Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILLES IT, AND PREVENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                   Prabhakar S., Tyagi J.S., Prasad H.K.;
"HLPMt-A target for differentiation of M.tuberculosis and M.bovis.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKK---EKAYAKAKKAEAKA-AKKA--KAEAKKYAKAAKAEKKEYAAA----- 46
                                                                                                                 Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                STRAIN=BCG / Tokyo;
Matsumoto S., Yukitake H., Matsuo T., Mineda T., Yamada T.;
"Identification of a novel protein generating bacterial slow growth
                                                                                              Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1988 (Rel. 08, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1.10 (Methylated DNA binding protein-2-H1) (MDBP-2-H1).
Gallus gallus (Chicken).
ENkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
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                   DNA-binding protein HU homolog (Histone-like protein) (Hlp) HUP OR HLP OR MDP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Repeat. BACTERIAL HISTONE-LIKE DOMAIN.
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199 A -> T (IN REF. 2).
21262 MW; 19FCE67885DFE6A8 CRC64;
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P02346; 1HUU.
InterPro; IPR000119; Bac DNAbind.
InterPro; IPR001136; Histone HI/H5.
Pfam; PP00216; Bac DNA binding; I.
PRINTS; PR00624; HISTONEH5.
ProDom; PD000945; Bac DNAbind; I.
SMART; SM00411; BHL; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 SVRKAATKAPAKKAAAKRPATKA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y18421; CAB46493.1; -.
EMBL; AB013441; BAA78330.1; -.
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                                                                      Mycobacterium bovis.
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205 AA;
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Matches 39; Conserv
                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                          NCBI_TaxID=1765;
                                                                                                                                                                                                             STRAIN=AN5;
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CONFLICT Query Match

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DOMAIN DOMAIN

H110\_CHICK
D H110\_CHIC
AC P08256;
DT 01-NUG-1
DT 15-UL-1
DE Histone
OS Gallus G
OC ENkaryot

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LARGE MOLECULES
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H1 WHEAT
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MEDLINE=91372983; PubMed=1894368;
MEDLINE=91372983; PubMed=1804368;
MEDLINE=91372983; PubMed=1804368;
Sliviansky L., Schouls L.M., van Embden J.D., Charon N.W.;
"Treponema phagedenis encodes and expresses homologs of the Treponema pallidum TmpA and TmpB proteins.";
Infect. Immun. 59.3685-3693(1991).
-i- FUNCTION: TMP MAY SERVE AS A PORIN OR TRANSPORT PROTEIN FOR
Perry M., Thomsen G.H., Roeder R.G.; "Genomic organization and nucleotide sequence of two distinct histone gene clusters from Xenopus laevis. Identification of novel conserved upstream sequence elements.";
                                                                                                                      SEQUENCE FROM N.A.

Perry M., Thomsen G.H., Roeder R.G.;
"Genomic organization and nucleotide sequence of two distinct histone gene clusters from Xenopus laevis: Identification of novel conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 KQLQSKDKAAAAKKKAPLAAEAKKPAAAAKKTAKSPKKKVSAAAKSPKKLKKPAKAAKS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEA----KYKAEAAKA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
                                                                                                                                                                                                                       Biol. Chem. 260:479-499(1985).
- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
- SUBCELLULAR LOCATION: Nuclear.
- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.8%; Score 109; DB 1; Length 209; 47.0%; Pred. No. 0.017; live 8; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 AA; 21242 MW; 8537E9272678DF1A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Spirochaetales; Spirochaetaceae; Treponema
NCBI_TaxID=162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001386; Histone_H1/H5. Pfam; PF00589; linker histone; l. ProDom; PD000373; Linkerhist_N; l. SWART; SM00526; H15; l.
                                                                                  . Mol. Biol. 185:479-499(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X03018; CAA26815.1; -. EMBL; M21287; AAA49767.1; -.
                                                                                                                                                                                                           upstream sequence elements.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reponema phagedenis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; F24510; HSXL1A.
HSSP; P08287; IGHC.
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173 PAKKTA 178
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P29720;
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1. 17.
6 X 9 AA TANDEM REPEATS OF [EA]-A-A-R-X-
A-A-E.
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TREPONEMAL MEMBRANE PROTEIN B.
17 X 5 AA TANDEM REPEATS OF K-A-A-[AKR]-
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Triticum estivum (Wheat).
Triticum estivum (Wheat).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.2%; Score 107; DB 1; Length 384; 47.1%; Pred. No. 0.04; ive 8; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6E94CBC74294DE8C CRC64;
SUBCELLULAR LOCATION: OUTER MEMBRANE-ASSOCIATED. SIMILARITY: TO TMPB OF T.PALLIDUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H1 WHEAT STANDARD; PRT; 238 AA. P27806; 01-801-992 (Rel. 23, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                    Antigen; Outer membrane; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.
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                                                                                                                                                                                                                                                                               EMBL; M58563; AAA27480.1; -.
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les 33; Conservative
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261
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237 AARKAAEEAA 246
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . protein; Nuclear protein; DNA-binding; Multigene family.
238 AA; 24222 MW; 2CBIC16899B65A27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBI_TaxID=1773;
                                                                                                  H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp) (21-kDa Huninin-2-binding protein).
HUP OR HLP OR LBP21 OR RY2986C OR MT3064 OR MTGY349.01.
Mycobacterium tuberculosis.
                 STRAIN=CV. Horoshirikomugi; TISSUE=Seedling;
MEDLINE=92020152; PubMed=1923777;
Yang P., Katsura M., Nakayama T., Mikami K., Iwabuchi M.;
"Molecular cloning and nucleotide sequences of cDNAs for histone land HIB variants from wheat.";
Nucleic Acids Res. 19:5077-5077(1991).
                                                                                                                                                                                                                                        Morisawa G., Meehi T., Iwabuchi M.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HISTONES HI ARB NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE HI/HS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٠<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.0%; Score 106.5; DB 1; Length 56.2%; Pred. No. 0.03; tive 5; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; LinkerhIst_N.
Pfam; PF00538; linker histone; I.
PRINTS; PR00624; HISTONEH5.
ProDom; PD0000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X59872; CAA42529.2; -.
                                                                                                                                                                                                              STRAIN=cv. Horoshirikomugi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity
36; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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197 AKKA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 AKEA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chromosomal
                                                                                                                                                                                             REVISIONS.
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DBH_MYCTU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buxopean Boinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1997) to the SWISS-PROT data bank.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKRAYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                            STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Deloher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 akkvakkapakkatkaakkaatkaparkaatkapakkaatkapakkavkatkspakkvtk 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of Mycobacterium tuberculosis clinical and
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prasad H.K., Annapurna P.S., Dey A.B., Tyagi J.S., Jain N.K.,
                     Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from Complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.9%; Score 106; DB 1; Length 214; 42.4%; Pred. No. 0.03; tive 5; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PRO0045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Repeat; Complete proteome.
DOMAIN 10 90 BACTERIAL HISTONE-LIKE DOMAIN.
DOMAIN 101 214 DEGENERATE REPEATS REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 AVKKTAVKASVRKAATKAPAKKAAAKRPATKA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; MT3064; -...
Tuberculist; Rv2986c; -...
InterPro; IPR000119; Bac DNAbind.
InterPro; IPR001386; Histone H1/H5.
Pfam; PF00216; Bac DNA binding; 1.
PRINTS; PR00624; HISTONEHS.
ProDom; PD000945; Bac DNAbind; 1.
SMART; SM00411; BHL; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 71-86, AND DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z83018; CAE05427.1; -. EMBL; AE007127; AAK47393.1; -HSSP; P02346; 1HUU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Savita P.;
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4

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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protein search, using sw model 1 OM protein

March 10, 2003, 12:15:01 ; Search time 34.9494 Seconds
 (without alignments)
 389.109 Million cell updates/sec Run on:

US-09-816-989A-4

Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

671580 segs, 206047115 residues Searched: Total number of hits satisfying chosen parameters:

671580

seq length: 0 seq length: 200000000 0B 0B Minimum | Maximum | Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL Database

sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\*
sp\_organelle:\*
sp\_phage:\*
sp\_phage:\*
sp\_lant:\*
sp\_rodent:\* sp\_archea:\* sp\_bacteria:\*

sp\_unclassified:\*
sp\_rvirus:\* sp\_virus:\* sp\_vertebrate:\* sp\_bacteriap:\* sp archeap:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

KIES			Description	Q8x965 escherichia	Q9cm70 pasteurella	Q8zqt6 salmonella	Q9wwx1 pseudomonas	Q8z8c1_salmonella	Q937k4 erwinia chr	Q8zgz2 yersinia pe	O01395 drosophila	O65794 triticum ae	Q92a67 listeria in	Q8y5w4 listeria mo	Q39576 chlamydomon	Q9xh19 triticum ae	Q98kg7 rhizobium l	Q9h8h4 homo sapien	O9h9fl homo sapien
COLUMNICO			a	596X8Ö	Q9CM70	08ZQT6	Q9WWX1	Q8Z8C1	Q937K4	Q8ZGZ2	001395	065794	Q92A67	Q8Y5W4	039576	09XHL9	Q98KG7	Q9H8H4	Q9H9F1
			DB	16	16	16	0	16	~	16	Ŋ	10	16	16	10	10	16	4	4
			Match Length DB	394	389	407	372	376	395	388	275	284	243	239	232	275	1341	198	467
	æ	Query	Match	42.3	40.4	39.8	39.1	39.1	38.3	37.4	36.3	36.1	35.8	35.6	35.3	35.1	35.1	34.7	34.7
			Score	132.5	126.5	124.5	122.5	122.5	120	117	113.5	113	112	111.5	110.5	110	110	108.5	108.5
		Result	No.	н	7	m	4	'n	9	7	80	σ	10	11	12	13	14	15	16

EMBL; AE005252; AAG55075.1; -. EMBL; AP002553; BAB34197.1; -.

	Q8xvn7 ralstonia s O61164 plasmodium	Q9swu3 triticum ae	Q9swu2 triticum ae	Q8y1f6 ralstonia s	Q9fp71 oryza sativ	Q9uv33 ascobolus i	Q52088 pseudomonas	Q84528 paramecium	Q8t5c8 plasmodium	Q45370 bordetella	. Q99kc2 mus musculu	Q90zd7 bufo bufo g	Q9uan1 drosophila	Q8rxd0 arabidopsis		Q9kj98 escherichia	Q9ndi9 plasmodium		Q99281 parechinus	093946 candida alb	Q91369 xenopus lae	Q9ru45 deinococcus	O18319 chironomus		7	Q25636 parechinus
Q9SWU1 Q9XHL8	Q8XVN7	Q9SWU3	Q9SWU2	Q8Y1F6	Q9FP71	Q9UV33	Q52088	084528	Q8T5C8	Q45370	Q99KC2	Q90ZD7	Q9UAN1	Q8RXD0	800860	Q9KJ98	6IQN6Ö	Q26947	099281	093946	091369	Q9RU45	018319	Q23784	C9V6S7	Q25636
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227	1200	236	237	345	755	213	298	311	1866	182	436	224	312	485	924	629	969	1128	166	212	229	581	233	243	607	180
34.3	34.2	34.0	34.0	34.0	34.0	33.5	33.2	33.2	33.2	32.9	32.7	32.6	32.6	32.6	32.6	32.4	32.4	32.4	32.1	31.8	31.8	31.6	31.5	31.5	31.5	31.3
107.5	107	106.5	106.5	106.5	106.5	105	104	104	104	103	102.5	102	102	102	102	101.5	101.5	101.5	100.5	99.5	99.5	66	98.5	98.5	98.5	86
17	19	21	22	23	24	52	56	27	28	5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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SEQUENCE FROM N.A.
STRAIN=015-14/ RIMD 0509952;
STRAIN=015-14/ RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T., Han C.-G., Ohtsubo E., Nakayama K., Minata T., Takami H., Handa T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2011).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21074935, PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glaener J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Membrane spanning protein, required for outer membrane integrity
(Membrane spanning protein TolA).
TolA OR 20907 OR ESC9774.
Bscherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                             394 AA.
                                                                                             PRT;
                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=83334;
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SEQUENCE FROM N.A.
RESULT 1
                                                     596X80
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STRAIN=LT2 / SGSC1412 / ATCC 700720;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MT-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9WWX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9WWX1
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAYAKAK-----KAEAKA---AKKAKAEAKKYAKAAKAEKKEYAAAEAKYK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBZQT6;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tol protein, membrane spanning protein.
TolA OR STWOATA
Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21145866; PubMed=11248100;
May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur "Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL, AE006136; AAK03052.1; -. 88.3460-3465(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                          6
                                                                                              Score 132.5; DB 16; Length 394;
Pred. No. 0.00053;
8; Mismatches 13; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 126.5; DB 16; Length 389;
Pred. No. 0.0017;
9; Mismatches 12; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pasteurella multocida.
Bacteria, Proteobacteria, gamma subdivision, Pasteurellaceae,
Pasteurella.
                                                          5B58D8E8230BDE28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389 AA; 42197 MW; B4032F2A2FD9E94B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                            389 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000533; Tropomyosin, PRINTS; PR0194; TROPOMYOSIN. Complete proteome.
                                                          394 AA; 40517 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.4%;
                                                                                                Query Match 42.3%;
Best Local Similarity 58.9%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 AEKAKADAEAAQRKA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                       ||||||:||:|
214 EKAAADKKAAEKA 226
                                                                                                                                                                                                                                                                  55 AKAAA-KEAAYEA 66
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                                       Complete proteome. SEQUENCE 394 AA;
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NCBI_TaxID=602;
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QBZQT6
QBZQT6
QBZQQ AC QBZQQ
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DDT 02-M
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MEDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 АКККАБАБААКАААБАКККАБАБААКААВАБАКККАПАБААКАААБАКККАПЛАААКК.--- 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96198174; PubMed=8626299;
Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.;
"The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of the cell envelope.";
J. Bacteriol. 178:1699-1706 (1996).
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Characteratization of an OprL null mutant of Pseudomonas putida."; J. Bacteriol. 178:5836-5840(1996).
EMBL; X74218; CAB50780.1; -
EMBL; X74218; CAB50780.1; -
PINTES; PRO0624; HISTONEHS.
PRINTS; PRO0624; HISTONEHS.
SEQUENCE 372 AA; 40133 WW; 87F49785ECC3COBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 407;
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Bacteria: Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.8%; Score 124.5; DB 16; Length llarity 47.8%; Pred. No. 0.0026; Conservative 6; Mismatches 10; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 AA; 41865 MW; 2534352116602D75 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 AAAEAKYKAEAA------KAAAKEAA
                                                                                                                                                                                                                                                                                                                       EMBL; AE008730; AAL19691.1; -.
InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
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                                                                                                                                                                                                                                                                                    Nature 413:852-856(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
ses 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 407 AA;
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NCBI_TaxID=556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                             1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKA--EAAKAA 58
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Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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       DB 2; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 39.1%; Score 122.5; DB 16; Length Best Local Similarity 51.3%; Pred. No. 0.0036; Matches 40; Conservative 4; Mismatches 13; Indels
    39.1%; Score 122.5; DB 2; Length ilarity 51.5%; Pred. No. 0.0035; Conservative 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 AA; 38804 MW; EC21F2C4767A8A42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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EMBL; AL627268; CAD05209 1; -

THCEFPO; IPRO0104; AHTIFreeze 1.

PRINTS; PRO0308; ANTIFREEZEI.

PRINTS; PRO1574; TUBBYPROTEIN.
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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TOLA.
Brwinia chrysanthemi.
                              Similarity
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                                                                                                                                                                                                                              205 AEDAKKKA 212
                                                                                                                                                                                    59 AKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella.
NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tola protein.
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                                                 35;
Query Match
Best Local S
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Matches
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0828C1
01-M
DT 01-M

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11D 09377
AC 09377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.3%; Score 120; DB 2; Length 395;
Best Local Similarity 54.1%; Pred. No. 0.0061;
Matches 40; Conservative 9; Mismatches 13; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKE-----KAYAKAKK-----AEAKAAKKAKAEAKKYAKAAKAE-KKEYAAAEAK 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yersinia pestis.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                    Ray M.C., Vianney A., Cotte-pattat N., Lazzaroni J.; "characterization of the Erwinia chrysanthemi tol-pal genes."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ297885; CAC82708.1; - SEQUENCE 395 AA, 41601 MW; 3COCIDC12E181013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 37.4%; Score 117; DB 16; Length 388; Best Local Similarity 49.3%; Pred. No. 0.011; Matches 33; Conservative 10; Mismatches 18; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 AA; 40424 MW; 81447B04B30A7E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last seque
01-UNN-2002 (TrEMBLrel. 21, Last anno
11-ADA collicin import membrane protein.
TOLA OR YPO1123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         001395;
01-JUL-1997 (TrEMBLrel. 04, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ414146; CAC89966.1; -.
InterPro; IPR000104; Antifreeze.1.
PRINTS; PR00308; ANTIFREEZEI.
COMPLETE protecome.
SEQUENCE 388 AA; 40424 MW; 8144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / BIOVAR ORIENTALIS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 KKAEAA-AAAKKAA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 YKAEAAKAAAKEAA 63
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 KAAADAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 AAAKEAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=632;
                          STRAIN=3937;
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4,

1,

2; Gaps

21; Indels

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2 KKYAKKEKAYAKAKAEAKAAKK--AKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAA 59
  6; Mismatches
                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 294:849-852(2001).
BMBL, ALS96170, CAC97285.1; ..
Listilist, LIN02055, ..
InterPro; IPR002482; LysM.
Pfam, PF01476; LysM; LysM; Hypothetical protein; Complete pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / SEROVAR 6A;
                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein lin2055.
  Matches 32; Conservative
                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listeriaceae; Listeria.
NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria innocua.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 KEKAAAEA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 AKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                        01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                      01-DEC-2001
                                                                                                                                                                    212 K 212
                                                                                                                            60 K 60
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OBYSWA
AC OBYSW
DT 01-MA
DT 0
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                                                                                                                                                                                                                                                                                                           -! STRILLARITY).
-! SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
-!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
EMBL; UBS627; AABS1369.1; -
FlyBase; FBGN0020732; Dhyd\mst101(3).
Sperm; Repeat; Multigene family.
DOMAIN 64 255 13 X 16 AA APPROXIMATE TANDEM REPEATS OF
X-[KQ].-K-C-[AE]-E-X-A-[X]-K-X-X-X-
                                                                                                 Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AKKEKAYAKAKKAEAKAAKKAK--AEAKKYAKAAKAE-------KKEYAAAEAK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lilliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99249625; PubMed=9588026; Mikami K., Meshi T., Iwabuchi M.; Aroka K., Ohtsubo N., Fujimoto Y., Mikami K., Meshi T., Iwabuchi M.; Pupase sud function of the wheat H1 promoter with S phase specific activity."; Palant Cell Physiol. 39:294-306 (1998). EMBL; D87064; BAA25203.1; HSSP; P02259; HST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 113.5; DB 5; Length 275;
Pred. No. 0.015;
3; Mismatches 15; Indels 17,
                                                                                                                                                                                                                                                                                (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 284;
                                                                                                                                                                                                                                Neesen J., Heinlein U.A.O., Buenemann H.,
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76BAA7B2A2DF732C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29159 MW; 5165A2B922BCBA4E CRC64;
01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 113; DB 10;
Pred. No. 0.017;
                                       Axoneme-associated protein MST101(3).
MST101(3) OR DHMST101.
Drosophila hydei (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000637; AT hook.
InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02178; AT hook; 1.
Pfam; PF02178; AT hook; 1.
ProDom; PD000338; linker histone; 1.
SMART; SM00384; AT hook; 1.
SMART; SM00526; H15; 1.
SEQUENCE 284 AA; 29159 MW; 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [AE]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 AA; 30436 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.3%;
Local Similarity 52.7%;
tes 39; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.1%;
52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, 01-MAR-2002 (TrEMBLrel. 20, Histone H1.
                 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum (Wheat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 KCAEAAK-KEKEAA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 YKAEAAKAAAKEAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       065794;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Nordsiek G., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simose N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAE--AKYKAEAAKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein lmo1941.
LMO1941.
Listeria monocytogenes.
Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillales,
Listeriaceae, Listeria.
                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 35.8%; Score 112; DB 16; Length 243; Local Similarity 47.1%; Pred. No. 0.018; les 32; Conservative 11; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ll protein; Complete proteome.
243 AA; 25963 MW; 6B2493D143B159D1 CRC64;
                                                                                                               (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Kawashima K., Kimura T.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Steinhoff S.; Steinhoff S.; Structural and functional characterization of histone H1 from animal "Structural and functional characterization of histone H1 from animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAYAKAKK----ABAKAAKKAKAKAEAKKYAKA---AKAEKKEYAAAB 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
MCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.1%; Score 110; DB 10; Length 275; ilarity 48.7%; Pred. No. 0.03; Conservative 5; Mismatches 20; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPROJECT HISTONE HI/HS.
INTERPRO; IPR0013216; Linkerhist N.
Pfam; PF00538; linker histone; 1.
PRINTS; PR00624; HISTONEHS.
PRODOM; PD000373; Linkerhist N; 1.
SMART; SM00526; HIS; 1.
SEQUENCE 275 AA; 27793 MW; B96DB4B710FF188F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and plant cells.";
Theels (1998), University of Goettingen, Humboldtallee.
ERBL; B707024; AAD41007.1; -.
HSSP; P02259; 1HST.
                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein mll1482.
                                                                                                                                                                                                                                                                                                                     275 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1341 AA.
                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Histone H1 WH1B.1.
Triticum aestivum (Wheat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 PKGPPAKAAKTSAKDA 226
                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 AK-YKAEAAKAAAKEA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                              46 AEAKYKAEAAKAAAKEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                     Q9XHL9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q98KG7
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Q98KG7
                                                                                                                                                                                                                                                       RESULT 13
Q9XHL9
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                                                                                                           MEDILINE-21537279; PubMed=11679669;
A Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
A Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chercuani F., Couve E., de Daruvar A., Dehoux P.,
A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
A Gautier L., Geobel W., Garcia-Lopez N., Hain T., Hauf J., Dackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,
A Nordaiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T., Schmitt R.;
Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 AKKAAEEKAAAEEKKAAAEEKKAAAEKKAGEDAVKAANAKKEGEAAEE---KAAADK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Gaps
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Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.6%; Score 111.5; DB 16; Length
46.4%; Pred. No. 0.02;
ive 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; ALS91991; CAD0019.1; -.
ListiList; LM001941; -.
ListiList; LM001941; -.
InterPro; IRR002482; LysM.
SPfam; PF01476; LysM; 1.
SWART; SM00257; LysM; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 239 AA; 25836 MW; 72E59D576E0D7832 CRC64;
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SEQUENCE 232 AA; 24693 MW; 2D006AE44ABFA037 CRC64;
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Last annotation update)
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(TrEMBLrel. 01, I
(TrEMBLrel. 20, I
                                                                                              STRAIN=EGD-E / SEROVAR 1/2A;
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Best Local Similarity 46.44
Matches 32, Conservative
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Best Local Similarity 50.0
Matches 39; Conservative
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163 AAEKAAAE 171
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   NCBI_TaxID=1639;
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Histone H1.
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A ISOGIA T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

I Rogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Nishikawa T., Nagi K., Sugano S., Takahashi-Fujii A., Hara H.,

Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

A Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

A Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

I Submitted (AUG-2001) A. Pook.

I InterPro; IPR000637; AT hook.

SMART; SM00384; AT hook.

SEQUENCE 198 AA; 21353 MW; 46F43602BC12487B CRC64;
                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKE---KAYAKAK-KAEAKAAKKAKAEAKKYAKA---AKAEKKEYAAAEAKYKAE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MUN-2001 (TrEMBLrel. 17, Last annotation update)
CDNA FLJ13629 fis, clone PLACE1011056, weakly similar to histone H1, gonadal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Euteria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                 Query Match 35.1%; Score 110; DB 16; Length 1341;
Best Local Similarity 53.5%; Pred. No. 0.14;
Matches 38; Conservative 9; Mismatches 16; Indels 8
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Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL, PAP002997; BAB48847.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 1341 AA; 138670 MW; 79C5D8149C969BC8 CRC64;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2001 (TrEMBLrel. 17,
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nes 36; Conservative
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1255 ADAKAAAEQQA 1265
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Search completed: March 10, 2003, 12:25:56 Job time : 35.9494 sec8

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

March 10, 2003, 12:15:01; Search time 34.3924 Seconds (without alignments) 255.712 Million cell updates/sec

US-09-816-989A-4 313 score: Title: Perfect

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 segs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

| SIDS2/gcgdata/geneseq/geneseqp\_emb1/AA1982.DAT:+
| SIDS2/gcgdata/geneseqy\_emb1/AA1982.DAT:+
| SIDS2/gcgdata/geneseqy\_emb1\_AA1983.DAT:+
| SIDS2/gcgdata/geneseqy\_emb1/AA1984.DAT:+
| SIDS2/gcgdata/geneseqy\_emb1/AA1986.DAT:+
| SIDS2/gcgdata/geneseqy\_emb1/AA1986.DAT:+
| SIDS2/gcgdata/geneseqy\_emb1/AA1986.DAT:+
| SIDS2/gcgdata/geneseqy\_emb2-emb1/AA1980.DAT:+
| SIDS2/gcgdata/geneseqy\_emeseqp\_emb1/AA1990.DAT:+
| SIDS2/gcgdata/geneseqy\_geneseqp\_emb1/AA1991.DAT:+
| SIDS2/gcgdata/geneseqy\_emeseqp\_emb1/AA1991.DAT:+
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Copolymer molecula	Recombinant copoly	Peptide #10 used i	Amino acid polymer	Poly-Lys-Ala used	Nucleic acid trans				
	ΙD		AAY82575	AAY82576	AAY82577	AAY82573	AAR06445	AAY98499	AAY59044	AAU04289	AAB45852
	08	21	21	21	21	21	1	21	21	22	22
	Query e Match Length DB ]	99	77	86	109	26	154	100	100	100	100
ф	Query Match	100.0	90.3	85.6	73.0	63.3	41.4	40.9	40.9	40.9	40.9
	Score	313	282.5	268	228.5	198	129.5	128	128	128	128
	Result No.	1	7	е	4	S	9	7	ω	60	10

Recombinant copoly	Copolymer molecula	Listeria monocytog	Mycobacterium bovi	Human protein segu	Human DNA modifica	Human protein segu	M. tuberculosis hi	M. tuberculosis hi	Copolymer molecula	Plasmodium yoelii	Amino acid sequenc	Synthetic helical	Novel human diagno	Zuotin. Saccharom	Human zuotin prote	S cerevisiae apopt	Nucleic acid (NA)	E	Trypanosoma cruzi	Haemophilus influe	Trypanosoma cruzi	Bacillus sp alkali	Drosophila melanog	Quail H1 histone p	Trypanosoma cruzi	Streptococcus pneu	C albicans apoptos	#295	Protein #2883 enco	rain	#289		Human protein SEQ	High affinity macr
AAR06446	AAY82572	ABB49123	AAB20575	AAB95499	AAU03592	AAB94309	AAY34055	AAY57353	AAY82571	AAB24128	AAY14928	AAR25206	ABG28693	AAW30256	AAY32954	AAG70739	AAW24449	ABB63276	AAR84568	AAU35623	AAR84565	AAG80266	ABB62173	AAY76981	AAR84569	AAW14549	AAG70868	ABB35445	ABB20884	AAM56269	AAM16458	AAM04187	AAM78825	AAR28871
11	21	23	21	22	22	22	20	21	21	21	20	13	22	18	20	22	18	22	16	22	16	23	22	21	16	18	22	22	22	22	22	22	22	13
106	45	239	205	198	279	467	214	214	35	1507	223	140	334	433	433	433	46	299	643	829	564	859	607	219	472	160	427	617	617	617	617	617	1026	46
39.0	38.5	35.6	35.3	34.7	4.	4.	33.9	33.9	ω.	33.5	ë.	m.	32.9	ď	ď	32.7	ď	ď	ď	ď	32.1	ä	31.5	ä	ö	ö	30.4	30.4	0	30.4		0	30.4	30.0
122	120.5	111.5	110.5	108.5	108.5	108.5	106	106	105.5	105	104.5	104	103	102.5	102.5	102.5	102	102	101.5	101	100.5	66	98:2	96	95.5	95	95	95	95	95	95	95	95	94
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

AAY82574 standard; peptide; 66 AA. 28-JUL-2000 (first entry) AAY82574; 

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.

glatiramer acetate, autoimmune disease, antiarthritis, neuroprotective, osteopathic; immunosuppressive, antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease, chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; draves disease; dulliain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; Copolymer; molecular weight marker; TV-marker; immune disease; pemphigus vulgaris; systemic lupus erythematosus

Unidentified

WO200018794-A1

06-APR-2000.

99WO-US22402 24-SEP-1999;

98US-0101693. 25-SEP-1998;

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

CO LTD

98US-0101693.

24-SEP-1999; 25-SEP-1998;

06-APR-2000.

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                                                                                                                                                                                                                     AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight onlypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune hypochiditis, autoimmune mammal and propertion in the conditions and an ammental autoimmune ophoritis, autoimmune thyroiditis, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uvecretinitis, Crohis disease, chronic minus thrombocycopaenia purpura, colitis, crontact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barrers syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antianaemic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crown sideases; chronic immune thrombocytopeenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                          Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 313; DB 21; Length 66; 100.0%; Pred. No. 3e-24; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY82575 standard; peptide; 77 AA.
                                                                                                                                                                               Claim 10; Page 14; 72pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecular weight markers.
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                                                               WPI; 2000-317499/27.
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                     Lis D;
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WO200018794-A1

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or mutibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune cue uveoretinits, crohn's disease, choonic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriaais, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
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                                                                                                                                                                                                                                                                                                                Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous glatiramer acetate molecules, which makes them ideal for use as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.3%; Score 282.5; DB 21; Length 77; 84.4%; Pred. No. 3.6e-21; ive 0; Mismatches 1; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY82576 standard; peptide; 86 AA.
                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 14; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecular weight markers.
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                                                                                                                                                         (YEDA ) YEDA RES & DEV
(TEVA-) TEVA PHARM USA
                                                                                                                                                                                                                                                                      WPI; 2000-317499/27.
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28-JUL-2000 (first entry)

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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of an amino acid composition corresponding to the copolymer. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antichody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, dullain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physpetides which are analogous to molecular weights and physpetides which are analogous to molecular weights.
                    Crohn's disease, chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
inflammatory condition; multiple sclerosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                 (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
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                                                                                                                                                                         WO200018794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                   Lis D;
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3; ch . 85.6%; Score 268; DB 21; Length 86;
1 Similarity 75.6%; Pred. No. 1.1e-19;
65; Conservative 0; Mismatches 1; Indels 20; Gaps 1 AKKYAKKEKAYAK----AKKAEAK-----AAKKAKAEAKKYAKAAKAEKKEYAAAEAK 49 99 ------YKAEAAKAAAKEAAYEA 61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86 AA; Sequence Query Match Local Matches 셤 셤 8 ò

AAY82577 standard; peptide; 109 AA AAY82577; AAY82577 ID AAYE XX AC AAYE XX

RESULT 4

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Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                         Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                         Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                            (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or remithody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases. Such diseases include arthritic conditions, demyelinating diseases. Such diseases include arthritic conditions, demyelinating diseases. Such diseases include arthritic conditions, celevosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, crohn's disease, chonic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as have include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention Claim 10; Page 14; 72pp; English

109 AA; Sequence

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4
                                            43; Gaps
                                                                                                                             1 АККҮАККАЕКАУАККАКААКЕККАУАККЕАКАУКААБАКККАКАКАБАККУАКБААКККБА 60
Score 228.5; DB 21; Length 109;
Pred. No. 1.2e-15;
0; Mismatches 4; Indels 43;
                                                                                                                                                                       26 -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA
                                                                                     1 AKKYAKK-EKAYAKAKKA------EAKAAKKA----
  73.0%;
                      Best Local Similarity 56.9%;
Matches 62; Conservative
    Query Match
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10; Gaps

Indels

80.3%; Pred. No. 5.9e-13; ive 2; Mismatches 1;

53; Conservative

EAAYEA 66 EAAYEA 56

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63.3%; Score 198; DB 21; Length 56;

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1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60
                                                                    1 AKKYAKKEKAY --AEAKAE-KAAK--KAEAKAY-KAAEAKKK----AEAKYKAEAAKAAAK 50
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                                                                                                                                                                                                                   Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antianaemic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohi's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Gulllain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatitamer accetae related terrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatodia arthritis, osteoarthritis, autoimmune haemolytic annamia, autoimmune battering immune the present include arthritic conditions and annamia, autoimmune physicial include arthritis autoimmune haemolytic immune intermediate the properties and inflammatory conditions, and annamia, autoimmune physicial immune the properties and annamia in autoimmune physicial immune properties and annamia annamia.
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                                                                                                                                                                                       Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3
61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                  AAY82573 standard; peptide; 56 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 14; 72pp; English
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                                                                                                                    AAY82573;
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coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 U34691009, NRL B-19910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences. C sequences, originating from the 5' linker sequence, in order that the COP-1-77 contains oligonucleotide duplexes incoding the following respective RAK, AAK, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a compalinating disorder, e.g multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.4%; Score 129.5; DB 11; Length 154; 48.8%; Pred. No. 1e-05;
                                                                                                                                                                                                                                                              Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing genes encoding random polymers of aminoacid(s) - f
producing recombinant polypeptide(s) with biological and/or
immunological activity
                                                                                                                                                                                                    Recombinant copolymer 1-77, myelin basic protein analogue.
AAR06445 standard; protein; 154 AA
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89US-0312541.
                                                                                                                                  (first entry)
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N-PSDB; AAQ05664.
                                                                                                                                                                                                                                                                                                                                   multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           See also AAQ05665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-1990;
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17-FEB-1989;
                                                                                                                                  03-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP383620-A.
                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                 AAR06445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cook KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     certain
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The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36633-A36652 and peptide sequences AAY98456-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g. transporter systems are also used to cranspend animals (as models for human carcinogenesis or disease, cancer, and infection. The transporter systems are also used to cranspend animals (as models for human carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the callular and interiors. Incender in the cells of the nucleic acid into the callular and interiors.
                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent
               Gaps
                                                    KKYAKKEKAYAKAKKAEAKAAKKAKAEA-----KKYAKAAKAEKKEYAAAEAKYKA 52
                                                                       Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
40.9%; Score 128; DB 21; Length 100;
Best Local Similarity 62.7%; Pred. No. 9.3e-06;
Matches 42; Conservative 5; Mismatches 16; Indels
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               7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith
                                                                                                                                                                                                                                                                                                                                                                     Peptide #10 used in nucleic acid transporter system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 125-128; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cristiano RJ,
                                                                                                                                                                                                                                                        AAY98499 standard; Peptide; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                               || :| || || EAEEAEYKKYKKKAKKAKYK 117
                                                                                                                          EAAKA-----AAKEAAYE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                                                                                                    (first entry)
               39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-281993/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 AA;
                                                                                                                                                                                                                                                                                                                                  31-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6033884-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                             AAY98499;
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Matches
                                                                                                                          23
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The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to Scomponents: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety, (d) a moiety that is capable of moving or initiating movement through a nuclear membrane; and or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytopissm of the entire complex from the cell surface directly into the cytopissm of the entire complex of specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells animal model. The NTS can be used in vitro with tissue culture cells which allows the role of various nucleic acids to be studied by targeting specific expression into specifically targeted tissue culture cells. The last agent within the NTS avoids the problem of endosomal/lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Lys-Ala in positions 3 to 100 may be optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                  61
                                                                                                                                                                                                                                                                                                                          Nucleic acid transport system; NTS; cell surface receptor; cytosis; nuclear membrane; lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer.
40.9%; Score 128; DB 21; Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gottchalk S, Sparrow J,
                                                                                                                                                                                                                                                                                        Amino acid polymer seq ID NO: 64 of US5994109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Columns 123-124; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 3..100
                                                                                                                                                                                   AAY59044 standard; peptide; 100 AA.
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92US-0855389.
93WO-US02725.
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                                                                                                                                                                                                                                                        07-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-038262/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Misc-difference 3.
                                                      57 AAAKEAA 63
                                                                                        62 AKAKAKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5994109-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                    AAY59044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Gaps

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1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK 56

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                                                                                                                                                                                                                                                                                                                            Nucleic acid transport; cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 3..100
/note= "Lys-Ala in positions 3-100 may be present or
absent"
                                                             1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK
                   4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sparrow J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 100;
                16; Indels
                                                                                                                                                                                                                                                                                              Poly-Lys-Ala used in nucleic acid transporter system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 128; DB 22;
Pred. No. 9.3e-06;
5; Mismatches 16;
 Pred. No. 9.3e-06;
                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Column 131, 111pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                          AAU04289 standard; Peptide; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BAYU ) BAYLOR COLLEGE MEDICINE
62.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0167641.
92US-0855389.
93WO-US02725.
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1 Similarity 62.7%;
42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0462040.
                                                                                                                                                                                                                                                                    (first entry)
                  42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-365933/38
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 3
                                                                                                      57 AAAKEAA 63
                                                                                                                                   AKAKAKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1993;
                                                                                                                                                                                                                                                                  23-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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                                                                                                                                                                                                                                       AAU04289;
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                                                                                                                                   62
                Matches
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This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, appliepproteins, receptors, drugs, oncogenes, tumor antigens, tumor suppressors, viral antigens, drugs, oncogenes, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                     Nucleic acid delivery, nucleic acid transporter system, hormone, enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                    Nucleic acid transporter system peptide ligand SEQ ID NO 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WOO SLC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 128; DB 22;
Pred. No. 9.3e-06;
5; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 125-126; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cristiano RJ,
AAB45852 standard; Protein; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.9%;
                                                                                                                                                                                                                                                                                                                                                                                  92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                                                                                                95US-0460971.
                                                                                                                                                                                                                                                                                                                                                              93US-0167641.
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gottchalk S, Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-049093/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 AA;
                                                                                                                                                                                         bacterial antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAKEAA 63
                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-1993;
                                                                    21-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                14-DEC-1993;
                                                                                                                                                                                                                                                           US6150168-A.
                                                                                                                                                                                                                                                                                              21-NOV-2000.
                                  AAB45852;
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Matches
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4;

Gaps

4;

16; Indels

Local Similarity

Matches

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1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK 56

62 AKAKAKA 68

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To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subclomed from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NREL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences, originating from the S' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-19 contains oligonucleotide duplexes incoding the following segments: YKK, AAE, KAK, EKA, KRA, YEA, ARA KRA, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKAKKAEAKAAKKAK-AEAKKYAAKAAKAEKKEYAA--AEAKYKAEAAKA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control sdemyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                     Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.0%; Score 122; DB 11; Length 106; 55.1%; Pred. No. 3.9e-05; ive 6; Mismatches 21; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing genes encoding random polymers of aminoacid(s) - iproducing recombinant polypeptide(s) with biological and/or
                                                                                                                                        Recombinant copolymer 1-19, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Indels
                                AAR06446 standard; protein; 106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 12; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 55.1%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                  90EP-0301700
                                                                                                                                                                                                                                                                                                                                                                                   90US-0473845.
89US-0312541.
                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                        (REPL-) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       certain amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1990-255848/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           See also AAQ05664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ06446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion protein.
                                                                                                                                                                                                                                                                                                                                                  16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-1990;
17-FEB-1989;
                                                                                                    03-JAN-1991
                                                                                                                                                                                                                                                                                                               22-AUG-1990.
                                                                                                                                                                                                                                                                             EP383620-A.
                                                                                                                                                                                                                                            Synthetic.
                                                                   AAR06446;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cook KS;
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RESULT 11
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AAM82571 to AAM82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune hamolytic
                                                                                                                                                                                                                                                                                                                     glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosupressive; antithyrodic, antinflammatory; antidabetic; thyromimetic; newostatic; antipsoriatic; dermatological; antidanemic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; ornonic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anaemia, autoimmune oophoritis, autoimmune thyrolditis, autoimmune topophoritis, autoimmune thyrolditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                       Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                     Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                               AAY82572 standard; peptide; 45 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0101693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US22402.
                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-317499/27.
88 AEKAKAAYK 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gad A, Lis D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                        28-JUL-2000
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                                                                                                                                                             AAY82572;
                                                                 RESULT 12
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38.5%; Score 120.5; DB 21; Length 45;

45 AA;

Sequence Query Match

<u>ښ</u>

4; Gaps

58 AAK-EAAYE 65

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The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for relating specific articles, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin all monocytogenes and related organisms, and selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and sequence and related organisms for the treatment or prevention of infections by L. monocytogenes and related organismin of infections by L. monocytogenes and related organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P, Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                     7;
                        6; Indels
                                                                                                  1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAKEAAYEA 45
                                                           29 AKKYAKAAKAE--KKEYAAAEAK----YKAEAAKAAAKEAAYEA
  71.1%; Pred. No. 2.2e-05;
ive 0; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; SEQ ID No 1828; 192pp; French.
                                                                                                                                                                                                                                                                                                                                           Listeria monocytogenes protein #1827
                                                                                                                                                                                                            ABB49123 standard; Protein; 239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-2000; 2000FR-0004629
                                                                                                                                                                                                                                                                                                  (first entry)
                   32; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200177335-A2.
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                                                                                                                                                                                                                                                        ABB49123;
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ABB49123
                   Matches
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DB 23; Length 239;

Score 111.5; DB Pred. No. 0.001;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Mycobacterium DNA binding protein 1 immunogenic for pathogenic acid-fast bacteria for diagnosis, treatment and prevention of diseases
                                         7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the Mycobacterium bovis BCG strain mycobacterium DNA binding protein 1 (MDP1), which has immunogenicity against pathogenic acid-fast bacteria. The MDP1 protein can be used idiagnosis and treatment of diseases involving pathogenic acid-fast bacteria, such as tuberculosis, Mycobacterium avium intracellular complex (MAC) and Hansen's disease.
                                                                                                                                                                                                                                                                                                  Mycobacterium bovis BCG strain; mycobacterium DNA binding protein 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKK---EKAYAKAKKAEAKA-AKKA--KAEAKKYAKAAKAEKKEYAAA------ 46
                          1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKY----AKAAKAEKKEYAAAEAKYKAEAAK
                                                                                                                                                                                                                                                                                                               MDP1; slow growing acid-fast bacterium protein; immunogenicity; pathogenic acid-fast bacterium; diagnosis; tuberculosis; MAC; Mycobacterium avium intracellular complex; Hansen's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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47.0%; Pred. No. 0.0011;
tive 5; Mismatches 22; Indels
13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                      Mycobacterium bovis BCG strain MDP1 protein SEQ ID NO:2.
                                                                                                                                                                                   AAB20575 standard; Protein; 205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 2A; 62pp; Japanese.
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32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        such as tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YAMA/) YAMADA T. (MATS/) MATSUMOTO S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-543393/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium bovis
                                                                                                             163 AAAEKAAAE 171
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                                                                                  AAAKEAAYE 65
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                                                                                                                                                                                                               AAB20575;
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The present invention describes primer sets for synthesising 5602

(ull-length cDNAs defined in the specification. Where a primer set
comptises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
cligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence of the sequence of the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
che full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH0365 to AAH13628 and
AAH13613 to AAH13629 complement and no add sequences; and AAH13629 complement and no add sequences; and AAH13629 complement represent human and a did sequences; and AAH13629 to AAH13632
represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                      Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.7%; Score 108.5; DB 22; Length 198; 50.7%; Pred. No. 0.0016; tive 9; Mismatches 17; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hikawa T, Hayashi K, Saito K, Ye
Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID 18049; 2537pp + CD ROM; English.
                                                                                                                                                              Human protein sequence SEQ ID NO:18049.
                                      AAB95499 standard; Protein; 198 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ota T, Isogai T, Nishikawa T,
Ishii S, Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                             27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                      (first entry)
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Best Local Similarity
Matches 36; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-318749/34.
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                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                  EP1074617-A2.
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                                                                              AAB95499;
RESULT 15
                   AAB95499
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Yamamoto J;

4;

Gaps

Conservative

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52 AEAAKAAAKEA 62
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77 AKAVRAKAKVA 87
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GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.

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                                        March 10, 2003, 12:26:10 ; Search time 19.6329 Seconds (without alignments) 141.764 Million cell updates/sec
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| Cgm2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| Cgm2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| Cgm2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
| Cgm2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
| Cgm2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
| Cgm2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
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110 US-09-816-989A-3

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US-09-864-761-3761
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US-09-815-242-5198
US-09-815-242-13765
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Maximum Match 100%
Listing first 45 summaries
  protein search, using sw model
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Sequence 90, Appl Sequence 48, Appl	Sequence 10314, A	Sequence 1164, Ap	Sequence 5197, Ap	Sequence 3, Appli	Sequence 2, Appli	Sequence 559, App	Sequence 5, Appli	Seguence 11, Appl	Sequence 9, Appli	Sequence 23, Appl	Sequence 100, App	Sequence 8, Appli	Sequence 8, Appli	Sequence 35241, A	Sequence 18, Appl	Sequence 10575, A	Sequence 4893, Ap	Sequence 46, Appl	Sequence 7, Appli	Sequence 5751, Ap	Sequence 6, Appli	Sequence 233, App	Sequence 960, App	Sequence 257, App
9 US-09-999-724-90 9 US-09-999-724-48	10 US-09-815-242-10314	10 US-09-925-300-1164	9 US-09-738-626-5197	10 US-09-124-280A-3	10 US-09-923-304-2	10 US-09-925-302-559	₽	10 US-09-893-238-11	_	9 US-09-820-843A-23	0	-		10 US-09-864-761-35241	10 US-09-876-889-18	10 US-09-815-242-10575	10 US-09-815-242-4893	_	_	9 US-09-738-626-5751	9 US-10-141-627-6	10 US-09-764-846-233	10 US-09-764-869-960	10 US-09-764-846-257
102	890	300	009	434	220	265		351	-						100	769	782					53	16	76
27.0	27.0	26.7	26.7	26.5	26.4	26.4	26.0	26.0	25.9	25.9	25.9	25.6	25.6	25.6	25.6	25.6	25.6	25.4	25.1	24.9	24.9	24.6	24.6	24.6
84.5 84.5	84.5	83.5	83.5	83	82.5	82.5	81.5	81.5	81	81	81	80	80	80	80	80	80	79.5	78.5	78	78	77	77	77
20	22	23	24	25	26	27	28	29	30	31	32	33	34	35	. 36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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APPLICANT: 134, DOTAS
APPLICANT: 154, DOTAS
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKY
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
FULE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 1001-1633
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1999-09-25
PRIOR PELING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIAN OFFICE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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1 Similarity 100.0%; Pred. No. 4e-23;
66; Conservative 0; Mismatches 0;
                                       Sequence 4, Application US/09816989A Patent No. US20020115103A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                  APPLICANT: Gad, Alexander
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Matches 66; Conserv
JS-09-816-989A-4
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; Sequence 5, Application US/09816989A

RESULT 2 US-09-816-989A-5

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Sequence 7, Application US/09816989A

| Sequence 7, Application US/09816989A
| Patent No. US20020115103A1
| GENERAL INFORMATION:
| APPLICANT: Lis, Doris
| TITLE OF INVENTION: COROLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE;
| TITLE OF INVENTION: AND FOR THERAPEUTIC USE
| TITLE OF INVENTION: AND FOR THERAPEUTIC USE
| FILE REFERENCE: 2609/60807-A-PCT-US
| CURRENT PFLLING DATE: 2001-03-23
| PRIOR FILING DATE: 1998-09-25
| PRIOR PAPLICATION NUMBER: 60/101,693
| PRIOR FILING DATE: 1999-09-24
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lis, Doris
TITLE OF INVENTION: COOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKAITILE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION UNMBER: US/09/816,989A
CURRENT APPLICATION UNMBER: 0010-03-23
PRIOR RILING DATE: 2001-03-23
PRIOR PILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENCHION VERSION 3.1
SEQ ID NO 3
LENGTH: 56
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US-09-816-989A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA 66
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80.3%; Pred. No. 1.6e-12;
tive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.0%; Score 228.5; DB 10
Best Local Similarity 56.9%; Pred. No. 4.7e-15;
Matches 62; Conservative 0; Mismatches 4
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APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.3
Matches 53; Conservative
                                                     RESULT 4
US-09-816-989A-7
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US-09-816-989A-3
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                                        APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: US/09/0807-A-PCT-US
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A;
CURRENT FILING DATE: 2001-03-23
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO S: 7
LENGTH: 77
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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT PAPLICATION NUMBER: US 0/9/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHING VEXEION 3.1
SEQ ID NO 6
LENGTH: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.3%; Score 282.5; DB 10; Length 77;
84.4%; Pred. No. 3.2e-20;
Live 0; Mismatches 1; Indels 11;
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85.6%; Score 268; DB 10;
Best Local Similarity 75.6%; Pred. No. 7.9e-19;
Matches 65; Conservative 0; Mismatches 1;
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APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Patent No. US20020115103A1
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Best Local Similarity
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US-09-816-989A-6
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Matches
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Sequence 1, Application US/09816989A

Patent No. US2002015103A1

GENERAL INFORMATION:

APPLICANT: Lis, Doris

APPLICANT: Lis, Doris

TITLE OF INVENTION: COOLUMER 1 RELATED POLYBEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: 60/101,693

PRIOR PILING DATE: 1998-09-24

PRIOR PILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 25
                                                                                                                                                                                                                                                                                                      ## Sequence 5, Application US/10184832

| Sequence 5, Application US/10184832
| Sequence 5, Application No. 220030022857A1
| Sequence 5, Application No. 220030022857A1
| GENERAL INFORMATION: COMPOSITIONS AND METHODS FOR THE | TITLE OF INVENTION: COMPOSITIONS AND WEIGHT DISORDERS, INCLUDING OBESITY | TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY | FILE REFERENCE: MP12001-056P1NM | CURRENT FILING DATE: 2002-06-28 | PRIOR APPLICATION NUMBER: 0202-06-28 | PRIOR APPLICATION NUMBER: 0203-06-28 | NUMBER OF SEQ ID NOS: 6 | SOFTWARE: FASELSEQ for Windows Version 4.0 | SEQ ID NOS: 6 | COMPOSITION NUMBER: PASELSEQ for Windows Version 4.0 | COMPOSITION NUMBER: PASELSEQ for Windows Version NUMBER: PASELSEQ for Windows Version 4.0 | COMPOSITION NUMBER: PASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKE-----KAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels 31; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 114; DB 9; Length 452;
Pred. No. 0.00087;
6; Mismatches 16; Indels
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56.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 56.59
Matches 39; Conservative
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                                                                                                                                  228 AEAKAATEAKRKA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus
US-10-184-832-5
                                                   54 AAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 AEAKAEAKE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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Squence 8, Application US/09820843A
Publication No. US2003003963A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEITILE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT PAPLICATION UNBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 AEEEAKAKAAEIAAOKAKOEAEAKAKUEAEAKAKAVAEAKAKAEAEAKAKAAAEAKAKAD 227
1 AKKYAKKEKAY--AKKAE-KAAK--KAEAKAY-KAAEAKKK----AEAKYKAEAAKAAAK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 372;
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NAME/KEY: misc feature

OTHER INFORMATION: outer membrane integrity protein (tolA)

NAME/KEY: misc feature

OTHER INFORMATION: gi|1573353
US-09-820-843A-8
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46.6%; Pred. No. 0.00034;
tive 10; Mismatches 22
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEP;
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR PAPLICATION NUMBER: 60/101,693
PRIOR PLING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENT NO
                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 2, Application US/09816989A
; Patent No. US200201115103A1
; GENERAL INFORMATION:
APPLICANT: Gad, Alexander
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                                                                                    61 EAAYEA 66
                                                                                                                                                                        51 EAAYEA 56
                                                                                                                                                                                                                                                                                                               RESULT 6
US-09-816-989A-2
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APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REFERENCE: 1000.1008c2
CURRENT APPLICATION NUMBER: US/10/051,643
FRIOR APPLICATION NUMBER: US/90/156,181
PRIOR PLING DATE: 1998-09-17
PRIOR PLING DATE: 1998-09-17
PRIOR PLING DATE: 1998-112-23
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FRASESEQ for Windows Version 3.0
SECTION 201
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APPLICANT: Obligation, Kari L.
APPLICANT: Tradic, Judith W.
APPLICANT: Tradic, John D.
APPLICANT: Xu, Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKARYOTES
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 06/201,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
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Pred. No. 0.0032;
4; Mismatches 20; Indels
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Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                    ; Sequence 201, Application US/10051643; Publication No. US20020197265A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i TYPE: PRTi ORGANISM: Mycobacterium vaccaeUS-10-051-643-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.4%;
52.2%;
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Matches 36; Conservative
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175 PAKKAATKA 183
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EAAYEA 66
                                              EAAYEA 35
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                                                                                                                                               US-10-051-643-201
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Sequence 27, Application US/09820843A
Publication No. US20030039963A1
Fublication No. US20030039963A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REPERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VETSION 3.0
SOFTWARE: PATENTING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-864-761-36182

Sequence 36182, Application US/09864761

Sequence 36182, Application US/09864761

Sequence 36182, Application US/09864761

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKEKAYAKAKKAEAK----AAKKAKAE-AKKYAKAAKAE-----KKEYAAAEAK 49
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                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                               32.3%; Score 101; DB 10; 34.8%; Pred. No. 0.026; tive 20; Mismatches 23;
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRALSEQ for Windows Version 4.0
SEQ ID NO 11216
LENGTH: 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
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                                                                                                                                                                                , TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-11216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
CTHER INFORMATION: tolA protein
NAME/KEY: misc feature
CTHER INFORMATION: gi|9556364
US-09-820-843A-27
                                                                                                                                                                                                                                                                                                                                                      23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 356
TYPE: PRT
ORGANISM: Vibrio cholerae
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | : |
129 KAEEQA 134
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US-09-820-843A-27
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CURRENT APPLICATION NUMBER: US/09/864,761

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1 AKKYAKKE-KAYAKAKK----AEAKAAKKAKAKAKAKA--AKAEKKEYAAAE 47
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OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 0.94

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN FERTL LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED THT: PL2036, EVALUE 2.00e-33

OTHER INFORMATION: EST_HUMAN HIT: BF445754.1, EVALUE 3.00e-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36182
LENGTH: 617
                      PRIOR APPLICATION NUMBER: US 50/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,356
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/180,312
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; Publication No. US20030021795A1
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Matches 32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-864-761-36182
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US-09-882-774-1
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Sequence 24, Application US/09820843A
Publication No. US20030039963A1
GENERAL INFORMATION:
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 201-03-30
NUMBER OF SEQ ID NOS: 118
SOFFWARE: PATENTIN Version 3.0
SEQ ID NO 24
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H
               APPLICANT: Hodges, Robert
TITLE OF INVENTION: Use of Coiled-Coil Structural Scaffold to Generate
TITLE OF INVENTION: Use of Coiled-Coil Structural Scaffold to Generate
TITLE OF INVENTION: Structure-Specific Peptides
FILE REPERBUCE: 003592-007
CURRENT APPLICATION NUMBER: US/09/882, 774
CURRENT APPLICATION NUMBER: US 60/211,892
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.0
SEQ ID NO.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 aakpaakpaakpaakpaakpaaktraaktraakpaakpaakptakaaakpatkpatkpaakaaa 221
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CTHER INFORMATION: polyhydroxyalkanoate synthesis protein PhaF;
NAME/KEY: misc_feature
;
OTHER INFORMATION: gi|9951352
US-09-843A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.6%; Score 92.5; DB 9; Length 309; Best Local Similarity 47.8%; Pred. No. 0.058; Matches 32; Conservative 2; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.9%; Score 93.5; DB 9;
45.8%; Pred. No. 0.096;
tive 11; Mismatches 18;
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Job time : 19.7758 secs
                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 45.08
Matches 27; Conservative
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US-09-820-843A-24
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LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                              March 10, 2003, 12:15:04 ; Search time 11.6962 Seconds
  (without alignments)
166.029 Million cell updates/sec
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                                                                                                                                                                    1 AKKYAKKEKAYAKAKKAEAK...........EAKYKAEAAKAAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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Sequence 5
Sequence 2
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-167-641C-64
US-08-460-971A-64
US-08-962-040-64
US-08-993-008A-5
US-08-923-008A-5
US-09-923-323-5
US-09-05-855-201
US-09-05-855-201
US-09-203-284A-2
US-08-293-284A-2
US-08-293-284A-2
US-08-216-894-2
US-08-115-746-8
US-09-115-746-8
US-08-116-07-4
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Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Sequence
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Sequence
Sequence
                 Sequence
                                                                                                                                                                                                                                                                                                                                                 Sequence 64, Application US/08460890A

Sequence 64, Application US/08460890A

Patent No. 599410A

Patent No. 599410A

APPLICANT: Smith, Louis C.

APPLICANT: Smith, Louis C.

APPLICANT: Gottchalk, Stephen

TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND

TITLE OF INVENTION: METHODS OF USE

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSES: Lyon

STREET: 613 Weet Lyon

STREET: Suite 4700

CITY: LOS Annell
                                                                                                                                                                                                                   5-08-446-201-3
5-08-127-499A-23
5-08-482-847-23
                                                                                                US-08-312-949-2
US-08-072-070-2
US-08-469-434-2
US-08-214-222-2
                                                US-08-247-491A-3
US-08-319-795-2
US-08-468-985-2
                                                                                                                                                                  US-08-467-852A-2
US-08-468-718-2
US-08-247-491A-2
                                                                                                                                                                                                                                                                    -08-403-379A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: storage
COMPUTER: IBM COMPALIA
COMPATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSIFCATION: 435
PRIOR APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
APPLICATION NUMBER: 22, 1993
APPLICATION NUMBER: 22, 1993
APPLICATION NUMBER: 32,327
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
TELERAX: (213) 955-0440
FILIERAX: 67-3510
                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK 56
                                                                  4
                                                                                                                                                                                                                                                                 Sequence 64, Application US/08460971A
Patent No. 6150168
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gristiano, Richard J.
APPLICANT: Gottchalk, Stephen
ITILE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be CTHER INFORMATION: present or absent.

US-08-460-971A-64
                                 Length 100;
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                                 Score 128; DB 3; Length 10
Pred. No. 4.9e-06;
5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
COMPUTER: BESCHARL
SOFTWARE: FASEESE (FOR WINDOWS 2.0
SOFTWARE: FASEESE (FOR WINDOWS 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,971A
FILING DATE: UNBER: 08/167,641
FILING APPLICATION: 435
PRIOR APPLICATION NUMBER: 08/167,641
FILING DATE: MACCH 19,1993
APPLICATION NUMBER: 07/855,389
FILING DATE: MACCH 19,1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MACCH 19,1993
ATTORNEY,AGENT INFORMATION:
NAME: WARDLEY, RICHARD J.
REGISTRATION NUMBER: 32,32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 212/063
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEY: 67-3110
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                 40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
                             Query Match
Best Local Similarity 62.7
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                             62 AKAKAKA 68
                                                                                                                                                             57 AAAKEAA 63
   US-08-167-641C-64
                                                                                                                                                                                                                                                         US-08-460-971A-64
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                                                                                                                                               4; Gaps
                                                                                                                                                                           1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK 56
                                                                                                                                                                                             OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER WIFORMATION: present or absent.
                                                                                                             40.9%; Score 128; DB 2; Length 100;
62.7%; Pred. No. 4.9e-06;
tive 5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                          Query Match
Best Local Similarity 62.77
Matches 42; Conservative
TOPOLOGY: linear
MOLECULE TYPE: peptide
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                          57 AAAKEAA 63
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1 AKKYAK-KEKAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA-AK
                                                          9 КАУАКАК-КАБАКААККАКАБАККҮАКА-АКАЕККЕУАААБАКҮКАБА-АКАЛАК 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIFICATION S14
PROG ATTON NUMBER: US 60/032,436
TILING DATE: 18-DEC-1996
ATTONEY/AGENT INPOMMATION:
NAME: Sullivan, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/POCKET NUMBER: 33,064
REGISTRATION NUMBER: 33,064
REFERENCE/POCKET NUMBER: 33,064
RELEPHONE: 303-499-8089
THELEPAK: 303-499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.5%; Score 117.5; DB 4; Best Local Similarity 65.5%; Pred. No. 2.8e-05; Matches 36; Conservative 5; Mismatches 11;
                                                                                                                                                                                                                                  Sequence 6, Application US/08993008A
| Sequence 6, Application US/08993008A
| Patent No. 6153596
| GENERAL INFORMATION:
| APPLICANT: Liotta, Dennis C. APPLICANT: Mey, Shiow-Jyi
| APPLICANT: Perros, John A. APPLICANT: Poll, Jan F. APPLICANT: Poll, Jan F. APPLICANT: Poll, Jan TITLE OF INVENTION: Polycationic Oligomers NUMBER OF SEQUENCES: 6
| CORRESPONDENCE ADDRESS: ADDRESSE: Greeni-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Greenlee, Winner and Sullivan STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-993-008A-5; Application US/08993008A; Sequence 5, Application US/08993008A; Patent No. 6183596; GENERAL INFORMATION: APPLICANT: Liotta, Dennis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant DE: peptide
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SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: not re.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                 57 AAAKEAA 63
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US-08-993-008A-6
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                                                          Gaps
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Sequence 10. 617554

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Getchalk, Stephen
TITLE OF INVENTION: MUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: MCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: MCLEIC ACID TRANSPORTER SYSTEMS AND STREET: 633 West Fifth Street
STREET: California
CCUTY: Los Angeles
STATE: California
CCUTY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-462-040-64
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Best Local Similarity 62.7%; Pred. No. 4.9e-06;
Matches 42; Conservative 5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.

ZIP: 90071-206

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BACARGE
COMPUTER: 18M Compatible
COMPUTER: FRAESEQ for Windows 2.0
SONTWARE: FRAESEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
APPLICATION NUMBER: 30,1978
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REFERENCE/DOCKET NUMBER: 32,327
R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 42; Conserva
                                                                                                                                                                                                                                         57 AAAKEAA 63
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111 AKKVAKKAPAKKATKAAKKAATKAPARKAATKAPAKKAYKATKAPAKKAVKATKSPAKKVTK 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-008-929-329-5

JG 508-929-329-5

J Sequence 5, Application US/08929329

J Setent No. 6120770

GENERAL INFORMATION:

APPLICANT: Adams, John H

APPLICANT: Rappe, Stefan

JTILE OF INVENTION: Vaccine Compositions

TITLE OF INVENTION: Vaccine Compositions

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSE: Barnes & Thornburg

STREET: 11 S Meridian

STATE: Indianapolis

STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/929,329
                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 106; DB 3;
Pred. No. 0.0014;
5; Mismatches 22
                                                                                         PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-PM 3006
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-909
TELEPAX: (619) 535-909
TELEPAX: (619) 535-909
TELEPAX: (619) 535-901
TELEPAX: (619) 535-901
TELEPAX: (119) 535-901
TELEPAX: (119) 535-901
TELEPAX: (119) 535-901
TELEPAX: (119) 535-901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 AVKKTAVKASVRKAATKAPAKKAAAKRPATKA 202
                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
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FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P
REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 9359
TELECOMMUNICATION INFORMATION:
"""TEPHONE: (177) 211-7745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (317) 231-7433 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.9
Query Match
Best Local Similarity 42.4
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-889-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46204
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Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cchavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 KAYAKAK-KAEAKAAKKAKAEAKKYAKA-AKAEKKEYAAAEAKYKAEA 54
                                                                                                                                                                                                                                                                           COMPUTER: BUJDY disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTONEY/AGENT INFORMATION:
NAME: SUllivan, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 33-95
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: 333-499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 4370 La Jolla Village Drive, Suite 700 CITY: San Diego STATE: California ZiW: 92122 COMPUTET:
             APPLICANT: Wey, Shiow-Jyı
APPLICANT: Karr, Joan F.
APPLICANT: Poly Jan F.
TITLE OF INVENTION: Polycationic Oligomers
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: winner and Sullivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                   ADDRESSEE: Greenlee, Winner and Sullivan
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 48 amino acid TYPE: amino acid STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS: not relevant not relevant
Petros, John A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.6'
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: not molecule TYPE: pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ANTI-SENSE: NO
US-08-993-008A-5
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                                                                                                                                                                                                                      STATE: CO
COUNTRY: US
ZIP: 80303
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APPLICANT:
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ORGANISM: Mycobacterium vaccae US-09-205-426-201
                                                    Query Match
Best Local Similarity 52.23
Matches 36; Conservative
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Best Local Similarity 52.2
Matches 36; Conservative
 MOLECULE TYPE: protein
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175 PAKKAATKA 183
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     US-09-095-855-201
                                                                                                                                                                                                                                                                                                          US-09-205-426-201
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WS-09-095-855-201

Sequence 201, Application US/09095855

Patent No. 6160093

APPLICANT: Tan, Paul

APPLICANT: Viser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections

NUMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                      3,
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYAKAKKAE----AKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAA 55
                                                                                                                                                                                              Score 105; DB 3; Length 1507;
Pred. No. 0.012;
6; Mismatches 14; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11000.1002c3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/095,855 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-UN-1997
APPLICATION NUMBER: 08/97,362
FILING DATE: 23-DEC-1997
ATONNEY AGENT INFORMATION:
                                                 TOPOLGGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFRENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                                                                                                              33.5%;
50.8%;
1507 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                              Query Match
Best Local Similarity 50.8
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
               amino acid
                                                                                                                                                                                                                                                                                                                                                                                1232 KKALK 1236
                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                              56 KAAAK 60
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US-08-929-329-5
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                                                                                                                  1 AKKYAKKEKAYAK---AKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKA 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Lockshin, Curtis
APPLICANT: Nich, Alexander
APPLICANT: Holmes, Todd
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
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FACULANT: WASSON, JAMES D.

APPLICANT: WASSON, JAMES D.

APPLICANT: WASSON, JAMES D.

APPLICANT: WASSON, JAMES D.

TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Diagnosis of Mycobacterial Infections FILE REFERENCE: 11000.1002c4

CURRENT APPLICATION NUMBER: US/09/205,426

CURRENT APPLICATION NUMBER: 09/095,855

EARLIER APPLICATION NUMBER: 09/095,855

EARLIER FILING DATE: 1998-06-11

EARLIER FILING DATE: 1998-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1996-08-29

NUMBER OF SEQ ID NOS: 208

SOFTWARE: PASSON WINDER: 1996-08-29

SOFTWARE: PASSON WINDER: 1996-08-29

SOFTWARE: PASSON WINDER: 1996-08-29

SEQ ID NO 201

LENGTH: 223
33.4%; Score 104.5; DB 4; Length 223; 52.2%; Pred. No. 0.002; tive 4; Mismatches 20; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.4%; Score 104.5; DB 4;
52.2%; Pred. No. 0.002;
tive 4; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08346849; Patent No. 5670483; GENERAL INFORMATION:
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Score 102.5; DB 2; Length 433;
Pred. No. 0.0061;
9; Mismatches 22; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KKYAKKEK------AYAKAK-KAEAKAAKKAKAEAKKYAKAAKAEKKEYAAA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.4%; Score 101.5; DB 2; Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANGSOMA CRUZI
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
COTTY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELEPHONIN, PROPAMATION:
TELEPHONIN: (202)672-5300
TELEPHAX: (202)672-5399
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08216894 Patent No. 5876734 GENERAL INFORMATION:
                                                                                                                                                                                                                                            LEMEPHONE: (617) 861-640
TELEFAX: (617) 861-640
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 amin
                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acide TOPOLOGY: li-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 32.7%;
Best Local Similarity 41.0%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 AKKKNKRAIRNSAKEADY 367
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amino acid
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-293-284A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-216-894-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-216-894-2
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Fatent No. 5955343

GENERAL INFORMATION:
APPLICANT: Thomes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORWED BY
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKYAKKEK-----AYAKAK-KAEAKAAKKAKAEAKKYAKAAKAEKKEYAAA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 102.5; DB 1; Length 433;
Pred. No. 0.0061;
9; Mismatches 22; Indels 15
                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLINGENT PAPELCATION WHERE: US/08/293,284A
PILING*BATE: 22-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTATION NUMBER: 22,592
REFERRICE/DOCKET NUMBER: MIT-6008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02173-4799

COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
          STATE: DESCRIPTION OF THE STATE OF THE STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32.7%;
Best Local Similarity 41.0%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 AKKKNKRAIRNSAKEADY 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4: 433 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 EAKYKAEAAKAAAKEAAY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-346-849-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-08-293-284A-2
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61 EAA 63
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                                                            2 KKYAKKEKAYAKAKKAEAKAAKKAKAKAEAKKYAKAAKA-EKKEYAAAEAKYKAEAAKAAAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KKYAKKEKAYAKAKAEAKAAKKAKAEAKKYAKAAKA-EKKEYAAAEAKYKAEAAKAAAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.4%; Score 101.5; DB 4; Length 564; Best Local Similarity 46.0%; Pred. No. 0.0099; Matches 29; Conservative 10; Mismatches 23; Indels 1.
                                                                                                                                                                                                                                                                           Sequence 2, Application US/09115746
Patent No. 6228601
GENERAL INFORMATION:
APPLICANT: Kitchhoff, Louis V.
APPLICANT: Cotau, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOWA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLLY & Lardner
STREET: 3000 K Street, N.W., Suite 500
1 Similarity 46.0%; Pred. No. 0.0099;
29; Conservative 10; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECHOMIN: (202) 672-5300
TELEPHONE: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-216-894-8
; Sequence 8, Application US/08216894
; Retent No. 5876/34
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 564 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-09-115-746-2
  Best Löcal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAA 393
                                                                                                                                                                               391 EAA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                         61 EAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EAA 63
                                                                                                                                                                                                                                                              US-09-115-746-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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5.1.3
Compugen Ltd.
version 5
GenCore
Copyright (c) 1993
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protein search, using sw model OM protein March 10, 2003, 12:15:04 ; Search time 22.5802 Seconds (without alignments) 327.825 Million cell updates/sec Run on:

US-09-816-989A-5

366 1 AKKYAKKEKAYAKKAEKAAK......EAKYKAEAAKAAAKEAAYEA 77 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues Searched:

283224

seq length: 0 seq length: 200000000 Minimum DB : Maximum DB : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	BB	ΩI	Description
 	150.5	41.1	421	7	JV0057	tolA protein - Esc
7	148	40.4		7	F90725	membrane spanning
9	148	40.4	394	7	G85576	membrane spanning
4	146	39.9	376	N	AG0592	prot
Ŋ	141.5	38.7	347	7	E83525	
9	141	38.5	372	7	G64064	outer membrane int
7	œ	37.7	1701	7	T09127	probable erythrocy
80		37.2	210	N	A25550	histone H1 - sea u
σ		36.7	219	7	E60110	repetitive protein
10		36.7	231	N	859589	histone H1 - Chlam
11		36.6	1128	~	T30296	R27-2 protein - Tr
12		36.3	328	~	A44993	cytosolic repetiti
13		35.7	388	~	AC0138	TolA colicin impor
14	130	35.5	1390	0	S51364	sperm tail-specifi
15		35.4	214	~	G70673	probable hupB - My
16		35.1	211	0	A28100	histone H1-beta, e
17		34.8	344	0	S34153	mst101-1 protein -
18		34.7	217	0	A26721	histone H1-gamma,
19		33.6	248	Н	HSUR1P	histone H1, gonada
20		33.6	433	N	S25194	ea
21		33.5	206	~	809388	histone H1 - sea u
22		33.2	220	~	A28456	histone H1.10 - ch
23	122.5	33.5	311	~	T17698	hypothetical prote
24		33.3	243	~	AE1689	
25	'n	33.2	239	0	AE1317	
56		33.2	384	~	B43592	
27	'n	32.9	284	0	T06241	Ξ
28	'n	32.4	241	7	JN0748	H1-I
29	118	32.2	206	Н	HSTR1R	histone H1 - rainb

190 AAALKKKAEAAEAAKKA 211 AAEAKYKAEAAKAAAKEAAYEA 77

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RESULT 2 F90725

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3 KYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAK-----AAKAEKK-EYA 55

probable translati	cgcr-4 protein - C	histone H1 (clone	histone H1.11L - c	hypothetical prote	conserved hypothet	histone H1.03 - ch	histone Hl.02 - ch	histone H1 - musco	outer membrane ant	tolA protein VC183	histone H1 homolog	histone H1.1 - Cae	histone H1.01 - ch	histone H1-5 [vali	h-caldesmon - chic
T11583	819113	T06257	B28456	T06636	E75383	D28456	HSCH1	S01262	F71283	A82152	S61926	T23778	A23055	S51660	A33430
N	N	N	~	N	7	0	Н	~	~	0	N	~	~	H	⊣
1403	265	288	225	924	581	224	218	218	325	356	182	208	218	226	771
32.2	32.1	32.1	31.6	31.6	31.1	31.0	30.7	30.6	30.5	30.5	30.3	30.3	30.3	30.2	30.2
118	117.5	117.5	115.5	115.5	114	113.5	112.5	112	111.5	111.5	111	111	111	110.5	110.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002
C;Accession: UV0057; B64810
R;Levengood, S. K.; Webster, R. E.
J. Bacteriol. 171, 6600-6609, 1989
A;Title: Nucleotide sequences of the tolA and tolB genes and localization of their productive by Reference number: UV0057; MUID:90078104; PMID:2687247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Modecule type: DNA
A; Residues: 1-421 < LEN>
A; Carperimental source: strain JM105
A; Experimental source: strain JM105
A; Note: the authors translated the initiation codon GTG for residue 1 as Val
A; Note: the authors translated the initiation codon GTG for residue 1 as Val
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: B64810
A; Accession: B64810
A; Accession: B64810
A; Residues: 1-421 < BLAT
COMMENT: TONA
A; Residues: 1-421 < BLAT
A; Residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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ilarity 53.7%; Pred. No. 0.00019;
Conservative 8; Mismatches 23;
tolA protein - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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A; Start codon: GTG
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Local Sim.
44;
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Nature 413, 848-852, 2001
Ajuthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
Ajuthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Feference number: AB0502; PMID:11677608
A;Accession: AG0592
A;Status: preliminary
A;Accession: AG0592
A;Residues: DNA
A;Residues: 1-376 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05209.1; PID:g16501979; GSPDB:GN00176
C;Genetics:
A;Gene: STY0793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Told protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
C.Species: Beeudomonas aeruginosa
C.Species: Decudomonas aeruginosa
C.Species: Deccession: E83525
R.Accession: E83525
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laxbig, K.; Lim, Natrie 406, 559-964, 2000
A.Title 406, 559-964, 2000
A.Title 406, 599-964, 2000
A.Title 500, MUD: 20437337; PMID: 10984043
A.Recession: E83525
A.Status: preliminary
A.Status: preliminary
A.Status: 1-347 <STO>
A.Residues: 1-347 <STO>
A.Residu
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C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: G64064; UC5212
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocahmann, S.D.; Scott, J; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidmann, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Ritle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAEAKKYAKAAKAEKK----EY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 0.00077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 146; DB 2;
Pred. No. 0.00038;
7; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 КККАКАБАККҮАКААКАЕККЕУАААЕАКУКАЕААКАААКЕАА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74
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    AKKYAKKEKAYAKKAEKAAKKAEAKA--

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 54.4
Matches 49; Conservative
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nes 45; Conservative
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Matches
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    membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain C.Species: Bscherichia coli C;Species: Bscherichia coli C;Species: Bscherichia coli C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: P90725 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: F90725 A;Getus: preliminary A;Molecule type: DNA A;Residues: 1-394 cHAX> A;Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GN00154 A;Residues: 1-394 cHAX> A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics: A;Gene: EC80774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        members spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain C; Species: Escherichia coli (; Species: Escherichia coli (; Species: Escherichia coli (; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Nov-2001 C; Accession: G85501 #sequence_revision 16-Feb-2001 #text_change 09-Nov-2001 C; Accession: G85501 Burland, V:; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Accession: G85576
A; Accession: G8576
A; Accession: G8; Accession: G8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AG0592

tolA protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18
CSpeciaes: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;AccesBion: AG0592
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D; Wain, J.; Churcher, th, T.; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L; White, N.; Farrar,
                                                                                                                                                                                                                                                                                                                             geno
                                                                                                                                                                                           o.
                 protein TolA [imported] - Escherichia coli (strain 0157:H7, substrain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 148; DB 2; Length 394;
Pred. No. 0.00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYA----KKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKKEYAAAEAKYKAEAAKAAA-KEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKKEYAAAEAKYKAEAAKAAA-KEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches 4
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R;Hoft, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.; Donelson, J.E.., Infect. Immun. 57, 1959-1967, 1989
A;Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.
A;Reference number: A60110; MUID:89277508; PMID:2659529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-219 <HOF>
C;Comment: This protein contains a series of tandem repeats, each fourteen residues in l<
C;Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Chlamydomonas reinhardtii
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 23-Jul-1999
C;Accession: S99589; S62122
R;Fabry, S.; Mueller, K.; Lindauer, A.; Park, P.B.; Cornelius, T.; Schmitt, R.
Curr. Genet. 28, 333-345, 1995
A;Title: The organization structure and regulatory elements of Chlamydomonas histone gen<sup>*</sup>
A;Reference number: S59581; MUID:96120862; PMID:8590479
                                                         sea urchins Lytechinus pictus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
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A;Cross-references: EMBL:U16726
A;Note: the authors did not translate the codon for residue 1
A;Note: Cornelius, T.; Schmitt, R.; Rabry, S.; Ford, C.; Lindauer, A.; Mueller, K.; Cornelius, T.; Schmitt, R. submitted to the EMBL Data Library, October 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Trypanosoma cruzi
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 02-Jun-2000
C;Accession: E60110
                                                                                                                                                                                                                                                                                                                                                                                                                                        96 KTEAQKARAAAKKAKLAAKKKEQKEKKAAKTKARKEKLAAKKAAKKAAKKVKKPAAKAKK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 ATKVAGDEKOKAAEATKVAKVAEAEKORAREATKVAEAEKOKAAEA 129
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                         KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYA-KAAKAEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAAK-AEKKEYAAAEA 59
                                                                                                        A,Accession: A25550
A,Molecule type: DNA
A,Residues: 1-210 <kNA)
A,Cross-references: GB:XX4488; NID:g9616; PIDN:CAA28177.1; PID:g9617
C,Superfamily: histone H1
C,Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
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                                                                                                                                                                                                                                                                                     Length 210;
                                                                                                                                                                                                                                                                                     37.2%; Score 136; DB 2; Length 21
53.3%; Pred. No. 0.0013;
tive 7; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repetitive protein antigen 27 - Trypanosoma cruzi (fragments)
                          Nucleic Acids Res. 14, 8121-8133, 1986
A, Title: Comparison of the late H1 histone genes of the A, Reference number: A25550, MUID:87040778, PMID:3022245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                histone H1 - Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 53.5%
The 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.7
Matches 38; Conservative
          R; Knowles, J.A.; Childs, G.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 PAKKAÁKKPAAKKAA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 TKVAEAGKOKAAEAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 KYKAEAAKAAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 KYKAEAAKAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: E60110
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                  probable erythrocyte-binding protein MAEBL - Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T09127
R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1235, 1998
A;Title: A family of chimeric erythrocyte binding proteins of malaria parasites.
A;Reference number: Z16577; MUID:9811593); PMID:9448314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
C;Accession: A25550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKA----EAKKYAKAA-KAEKKEYA--- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 62/1; 1648/1; 1674/2; 1697/1
C;Keywords: alternative splicing; cell binding; erythrocyte invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                  A;Experimental source: strain 1479
A;Note: the authors translated the codon CGT for residue 190 as Ala C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 37.7%; Score 138; DB 2; Length 1701; Best Local Similarity 54.4%; Pred. No. 0.0046; Matches 43; Conservative 8; Mismatches 16; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1701 - KAA>
A;Cross-references: EMBL:AF031886; NID:g2947227; PID:g2947228
A;Experimental source: subspecies yoelii; strain YM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.5%; Score 141; DB 2;
54.7%; Pred. No. 0.00088;
ive 7; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 KEYAAAEAKYKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1283 KKAEEEKKKAEAAKKAEEE 1301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 47; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: tolA
A;Start codon: GTG
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A, Gene: maebl
A, Accession:
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4; Gaps

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Cispecies: Yersinia postis
Cispecies: Yersinia postis
Cispecies: Versinia postis
Cispecies: Versinia postis
Cispecies: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
Cispecsion: AC0136 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
Cispecsion: AC0136 #sequence_revision N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E A; Title: Genome sequence of Yersinia postis, the causative agent of plague.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Drosophila hyde:
C;Species: Drosophila hyde:
C;Accession: S51364; S34154
R;Neesen, J.; Padmanabhan, S.; Buenemann, H.

Bur. J. Biochem. 225, 1089-1095, 1994
A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif representable high and an arranged species of Drosophila hyde:
A;Reference number: S51364; MUID:95045538; PMID:7957199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: AC0138
A;Batus: preliminary
A;Batus: preliminary
A;Residues: 1-388 «KUR»
A;Residues: 1-388 «KUR»
A;Coss-references: GB:AL590842; PIDN:CAC89966.1; PID:g15979190; GSPDB:GN00175
C;Genetics:
A;Genetics:
                                                                                                      1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAKA-EKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 KEKAYAKKAEKAAKKAEAKAYK----AAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYK 62
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A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
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Pred. No. 0.015;
            22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
35.7%; Score 130.5; DB 2;
Best Local Similarity 51.4%; Pred. No. 0.0054;
Matches 37; Conservative 10; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
         9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-1390 «NEE> A;Cross=references: BMB1:X73481 submitted to the EMBL Data Library, June 1993 A;Reference number: S34153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: FlyBase: FBgn0011816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.5%;
51.7%;
            Matches 39; Conservative
                                                                                                                                                                                                                                                        167 TKVÁBÁBKOKÁABÁ 180
                                                                                                                                                                                            60 KYKAEAAKAAAKEA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |: || :||
214 VEVAEKAAADAA 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S51364
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S51364
                                                                                                                                                                                                                                                                                                                                                     RESULT 13
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A; Description: The organization, structure and controlling elements of Chlamydomonas his A; Reference number: $62122
A; Reference number: $62122
A; Accession: $62122
A; Accession: $62122
A; A; Charactule 1-173, Pr. 174-231 < FAW>
A; Residues: 1-173, Pr. 174-231 < FAW>
A; Cross-references: EMBL:U16726; NID:9571479; PIDN:AAA98452.1; PID:9571480
A; Cross-references: EMBL:U16726; NID:9571479; PIDN:AAA98452.1; PID:9571480
C; Genetics:
A; Introns: 62/3; 101/3
C; Superfamily: histone H1
C; Reywords: chromosomal protein; DNA binding; nucleosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Trypanosoma cruzi
C.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 17-Mar-2000
C.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 17-Mar-2000
C.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 17-Mar-2000
R;Otsu, K.; Donelson, J.E.; Kirchhoff, L.V.
Mol. Biochem. Parasitol. 57, 317-330, 1993
A):Itle: Interruption of a Trypanosoma cruzi gene encoding a protein containing 14-aminc
A;Retence number: 220813; MUID:93165082; PMID:8381919
A;Accession: T30296
A;Accession: T30296
A;Accession: Lype: DNA
A;Residues: l-1128 AOTS-
A;Cross-references: EMBL:L04603; NID:9385171; PID:91256742; PIDN:AAA96494.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oytosolic repetitive antigen - Trypanosoma cruzi (fragment)

CiSpecies Irypanosoma cruzi

CiSpecies Irypanosoma cruzi

CiDate: 14-May-1993 #sequence_revision 14-May-1993 #text_change 02-Jun-2000

CiAccession: A44993

Roll Biochem. Parsaitol: 35, 127-136, 1989

A.Title: Structure and expression of two Trypanosoma cruzi genes encoding antigenic prot A; Accession: A4993; MUID:89364992; PMID:2475776

A; Accession: A44993

A; Reference number: A44993

A; Residues preliminary; not compared with conceptual translation

A; Residues: 1-328 cLAF>

A; Residues: 1-328 cLAF>

A; Residues: 1-328 cLAF>

A; Cross-references: GB:304016

C; Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKXAEA------KAYKAAEAKKKAKAEAKKYAKAAKAEK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                               Score 134.5; DB 2; Length 231;
Pred. No. 0.0018;
4; Mismatches 26; Indels 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.6%; Score 134; DB 2; Length 1128; 52.0%; Pred. No. 0.0067; Live 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 328;
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Pred. No. 0.0031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 KPKAAKPAKKTTKKAAAKPKAEKKPKAAAKPKA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 KEYAA-----AEAKYKAE-AAKAAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.3%;
                                                                                                                                                                                                                                                                                                                                               Query Match 36.7%;
Best Local Similarity 47.3%;
Matches 44; Conservative
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T30296
R27-2 protein - Trypanosoma cruzi
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Best Local Similarity 52.09
Matches 39; Conservative
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Best Local Similarity
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Gaps

2

us-09-816-989a-5.open.rpr

5

16; Gaps

3; Mismatches 23; Indels

Matches 45; Conservative

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Cidene: 17'0013

Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Davies, R.; Davies, R.; Davies, R.; Davies, S.; Hamlin, N.; Holroyd, S.; Raindream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

Ajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Sarrell, B.G.

Ajathors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

Ajathors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

Ajathors: Sqares, R.; Sulston, J.E.; Taylor, R.; Whitehead, S.; Barrell, B.G.

Ajathors: Draining the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230

Ajacession: G70673

Ajacession: G70673

Ajacession: G70673

Ajacession: G80283018; GB:AL123456; NID:93261671; PIDN:CAB05427.1; PID:91694845

Ajacesimental source: strain H37Rv

CjGenetics:
AjGene: hupb

CjSuperfamily: histone H1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable hupB - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                Ouery Match 35.4%; Score 129.5; DB 2; Length 214;
Best Local Similarity 45.7%; Pred. No. 0.004;
Matches 43; Conservative 4; Mismatches 28; Indels 19; Gaps
2 KKYAKKEK--AYAKKAEKAAKK----AEAKAYKAAEAKKKAKAEAKKYAKAAK----AE 50
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                                                                                                                                                                                                                                                                      571 KKKCEKAAKERKEAAEKKKCEEAAKKE 597
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Search completed: March 10, 2003, 12:28:28 Job time : 23.5802 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 10, 2003, 12:15:01 ; Search time 17.5443 Seconds
 (without alignments)
182.035 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-816-989A-5 366 1 AKKYAKKEKAYAKKAEKAAK......BAKYKAEAAKAAAKEAAYEA 77

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	
SUMMARIES	110	11101011111111111111111111111111111111
	DB	! ! ! ,
	Length	
	Query Match	
	nult Query No. Score Match Length DB ID	1 1 1 1 1 1
	Result No.	

	Description	P19934 escherichia	P50600 pseudomonas	P44678 haemophilus		-	Q08696 drosophila	P95109 mycobacteri	-	Q08695 drosophila					Q9u761 aedes aegyp		P08286 gallus gall		P40277 chironomus	Q08865 volvox cart	_	-		-					P27806 triticum ae	P09987 gallus gall			σ	P10771 caenorhabdi
SUMMARIES	ID	TOLA ECOLI	TOLA_PSEAE	TOLA_HAEIN	H1_LYTPI	DBH_MYCBO	MST2_DROHY	DBH_MYCTU	DBH MYCSM	MST1 DROHY	H1G STRPU	H1B_STRPU	RS6 AEDAL	H1 PARAN	RS6 AEDAE		H110_CHICK	TMPB_TREPH	H1C_CHITE	H12_VOLCA	H1_ONCMY	HIE CHITE	YDF3 SCHPO	H11L_CHICK	H1B_CHITE	H11_GLYSA	H103_CHICK	IF2 PROVU	H1 WHEAT	HI_CHICK	H1_ANAPL	ASR_KLEPN		H11_CAEEL
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	Query Match Length	421	347	372	210	205	1391	214	208	344	217	211	349	248	346	433	219	384	221	240	206	237	1403	224	232	233	223	917	238	217	217	139	325	207
	Query	41.1	38.7	38.5	37.2	35.5	35.5	35.4	35.2	34.8	34.7	34.3	34.3	33.6	33.6	33.6	33.5	33.2	32.9	32.4	32.2	32.2	32.2	31.6	31.4	31.1	31.0	31.0	30.9	30.7	30.6	30.5	30.5	30.3
	Score	150.5	141.5	141	136	130	130	129.5	129	127.5	127	125.5	125.5	123	123	123	122.5	121.5	120.5	118.5	118	118	118	115.5	115	114	113.5	113.5	113	112.5	112		111.5	111
	esult No.	-	7	e	4	ស	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22		24	25	26	27	28	53	30	31	32	33

P08284 gallus gall P16401 homo sapien P12957 gallus gall P40263 glyptotendi P02254 salmo trutt P06892 xenopus lae P40275 chironomus P57873 pasteurella P67873 pasteurella P40274 trypanosoma P40262 chironomus P40262 chironomus P40262 chironomus P60893 xenopus lae
H101 CHICK H15 HUMAN CALD CHICK H11 GLYBA H11 GLYBA H12 AKBULA H1A CHITB H1A CHITB H1A CHICK H11A CHICK H162 TRYCR H162 TRYCR H16 CHIPA
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218 225 233 233 209 232 833 218 218
2222233330 2222233 2839333333333333333333333333333
111 110.5 110.5 110.5 109.5 109.5 109.5 106.5 106.5
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# ALIGNMENTS

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MEDLINE=97113525; PubMed=8955385;
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                                                                                             Duan K.,
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TOLA HAEIN
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                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                             MEDLINE=99332679; PubMed=10404600;
Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.;
With its coreceptor, the C-terminal domain of Tola.";
Structure 7.711-72(1999).
-!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A
COLICINS (COLICINS A, E1, E2, E3, AND K). NECESSARY FOR THE
COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL
BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION
OF BACTERIOPHAGE DNA.
-!- SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAK-----AAKAEKK-EYA 55
                                                                                                                                                                                                                                                                                                                                                                                                                PDB; 1TCD; 20-MAY-99.
EcoGene; EG11007; tolA.
Transport; Protein transport; Bacteriocin transport; Transmembrane;
                                                                                                                                                                                                               AND LAMB. SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERIPLASMIC (POTENTIAL).
DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
10 X TANDEM REPEATS OF [ED]-X(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tola protein.
TOLA OR PA0971.
Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
        "TolA central domain interacts with Escherichia coli porins.";
EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.1%; Score 150.5; DB 1; Length 421; 53.7%; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transpuri, Frocess Complete proteome.
Repeat, Inner membrane, 3D-structure, Complete proteome.
nomain 1 13 CYTOPLASMIC (POTENTIAL).
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8B2F52B4B97C655E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 AAALKKKAEAAEAAAEARKKA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 AA; 43156 MW;
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EMBL; AE000177; AAC73833.1; -.
EMBL; D90713; BAA35405.1; -.
PIR; JV0057; JV0057.
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421
310
421
278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                       PIR; JV0057;
PDB; 1TOL; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas.
Lloubes R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN PAO;
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DOMAIN
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P50600:
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TOLA PSEAE
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                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

MEDLINE=204373737; PubMed=10984043;

MEDLINE=204373737; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE004530; AAG04360.1, -.
Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKKAEAKA----YKAAE-A 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 347;
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                            οĘ
Dennis J.J., Lafontaine E.R., Sokol P.A.; "Identification and characterization of the tolQRA genes
                                                                                                                                                             Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 347 PEKALFURGUAN 209 216 POLY-ALA. 347 AA; 37935 MW; EEDD4B04AA095945 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
PERIPLASMIC (POTENTIAL).
POLY-ALA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 KKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 141.5; DB 1
Pred. No. 0.00043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.18; Pred. No.
                                                     Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U39558; AAC44660.2; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    opportunistic pathogen.";
Nature 406:959-964(2000).
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                                                                                                                                 REVISIONS TO N-TERMINUS
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37
347
216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Potential).
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Tola OR H10383.
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DBH_MYCBO
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                                                                                                                                                                                                                                      Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 AKRLAAAAKQAEEEAKAKAAEIAAQKAKQEAEAKAKLEAEAKAKAVAEAK--AK-AEAEA 214
STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95550630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Wenter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fransport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                            Sen K., Sikkema D.J., Murphy T.F.;
"Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA and tolB genes.";
Gene 178:75-81(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
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A -> P (IN STRAIN 1479).
A -> R (IN STRAIN 1479).
A -> A (IN STRAIN 1479).
-> A (IN STRAIN 1479).
-> AKAAABAKAKA (IN STRAIN 1479).
-> F (IN STRAIN 1479).
-> F (IN STRAIN 1479).
-> V (IN STRAIN 1479).
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V STRAIN 1479).
V STRAIN 1479).
V STRAIN 1479).
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-> P (IN STRAIN 1479).
266ECF05C6C95544 CRC64;
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54.7%; Pred. No. 0.00049;
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PERIPLASMIC
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                                                                                                                                                                                                                                                                               Science 269:496-512(1995)
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372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY)
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SEQUENCE
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RESULT 4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                         Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYA-KAAKAEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 210 AA; 21746 MW; 08C38F64894007E2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                               Knowless J.A., Childs G.J.;
"Comparison of the late H1 histone genes of the sea urchins
"Comparison of the late H1 histone genes of the sea urchins
"Lytechinus pictus and Strongelocentrotus purpuratus.";
Nucleic Acids Res. 14:8121-8131(1986).
-I- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-I- SUBCELULAR LOCATION: NUCLear.
-I- SUBCELULAR LOCATION: UNCLear.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
16-OCT-2010 (Rel. 40, Last annotation update)
16-OCT-2010 protein HU homolog (Histone-like protein) (Hlp).
Wycobacterium bovis.
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53.3%; Pred. No. 0.00072;
cive 7; Mismatches 26; Indels
                                                                                  01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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210 AA
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                                                                                                                                                              Lytechinus pictus (Painted sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, P02259; 1HST.
InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhīst_N.
Pfam; PF00538; linker histone; I.
ProDom; PD000373; Linkerhist_N; I.
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87040778; PubMed=3022245;
                                                       06, Created)
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 KYKAEAAKAAAKEAA
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SEQUENCE FROM N.A.
STRAIN=ANS;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                       01-JAN-1988 (Rel.
                                                                                                                                                                                                                                                Lytechinus.
NCBI_TaxID=7653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1765;
                                                                                                                                             Late histone H1
                                                                                                                                                                                                                                                                                                                                                                      IISSUE=Embryo;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
                                                                                                                                                                                                                111 AKKVAK--KAPAKKATKAAKKAATKAPAKKAATKAPAKKAVKATKSPAKKVTKAVKKTAV 168
                                                                                                                         Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Prabhakar S., Tyagi J.S., Prasad H.K.; "HLPMt-A target for differentiation of M.tuberculosis and M.bovis."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-201 (Rel. 40, Last annotation update)
Axoneme-associated protein mst101(2).
MST101(2).
Drosophila hydei (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Mandibulata; Pancrustacea; Hexapoda;
Insecta; Prerygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBL_TAXID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKAYAKKAEKAAKKA--EAKAYKAA-----EAKKKAKAKAEAKKYAKAEKK 52
                                                                   STRAIN=BCG / Tokyo;
Matsumoto S., Yukitake H., Matsuo T., Mineda T., Yamada T.;
"Identification of a novel protein generating bacterial slow growth from Mycobacterium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE-95045538; PubMed-7957199;
Neesen J., Padmanabhan S., Buenemann H.;
"Tandemly arranged repeats of a novel highly charged 16-amino-acid motif representing the major component of the sperm-tail-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 35.5%; Score 130; DB 1; Length 205; Local Similarity 49.4%; Pred. No. 0.0019; es 42; Conservative 7; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: POSOUGE: HISTONE LIKE; 1.
DNA-binding; DNA condensation; Repeat.
DOMAIN 1 90 BACTERIAL HISTONE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 205 DEGENERATE REPEATS REGION.
199 199 A -> T (IN REF. 2).
205 AA; 21262 MW; 19FCE67885DFE6A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1391 AA
                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02346; 1HUU.
InterPro; IPR000119; Bac_DNAbind.
InterPro; IPR001386; Histone_H1/H5.
                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00216; Bac_DNA_binding; 1.
PRINTS; PR00624; HTGTONEHS.
ProDom; PD000945; Bac_DNAbind; 1.
SMART; SM00411; BHL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 KASVRKAATKAPAKKAAAKRPATKA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 EYAAAEAKYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                       EMBL; AB013441; BAA78330.1; -.
                                                                                                                                                                                                                                                                                                                                        EMBL; Y18421; CAB46493.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DROHY .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Q08696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
MST2_DROHY
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                                                                                                                                                                                                                                                                                                                                                                                                                            -!- DEMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
-!- POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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15-JUL-1999 (Rel. 38, Last sequence update)
16-JUL-1999 (Rel. 40, Last annotation update)
16-JUL-1999 (Rel. 40, Last annotation update)
16-JUL-1999 (Rel. 70, Last annotation update)
18-JUL-1999 (Rel. 70, Last annotation update)
18-JUL-1999 (Rel. 70, Last annotation)
18-JUL-1999 (Rel. 70, Last annotation)
18-JUL-1999 (Rel. 70, Last annotation)
18-JUL-1999 (Rel. 38, Letternologie)
18-JU
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MEDLINE=9825987, PubMed=9634230;
MEDLINE=9825987, PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holrcyd S.
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Sulston J.E., Taylor K., Whitehead S., Squares R.,
"Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KKYAKKEK--AYAKKAEKAAKK----AEAKAYKAAEAKKKAKAEAKKYAKAAK----AE
                                                              ŏ
                                                                                                     Drosophila hydei.";

Bur. J. Biochem. 225:1089-1095(1994).

-I. FUNCTION: POSSIBLE STRUCTURAL IN THE SPERM TAIL.

-I. SUBCELLULAR LOCATION: Cycoplasmic.

-I. TISSUE SPECIFICITY: TESTIS. PRIMARY SPERMATOCYTES AND EARLY
axoneme-associated protein family Dhmst101 form extended alpha-helical rods within the extremely elongated spermatozoa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.5%; Score 130; DB 1; Length 1391; 51.7%; Pred. No. 0.0087; cive 3; Mismatches 23; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572 KKKCEKAAKERKEAAEKKKCEEAAKKE 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 KK--EYAAAEAKYKAEAAK---AAAKE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                    SPERMATIDS
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SEQUENCE FROM N.A.
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Q08695;
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1D MST1_D

C 00815_D

C 01-FBB

DT 01-FBB

DT 01-FBB

DT 01-FBB

DT 01-FBB

C 00 MST101

C 00 BMST101

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   SO THE STANTANT OF STANTANT OF
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                                   Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., BoBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Savita P.;
Submitted (DEC-1997) to the SWISS-PROT data bank.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DHA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
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                                                                                                                                                                                                      "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSF; r. Triang, March 1986; -. A TIGR; MT3064; -. A TIGR; MT3064; -. BR Tuberculist; Rv2986c; -. BR Tuberculist; Rv2986c; -. BR InterPro; IPR00119; Bac_DNabind.

BR InterPro; IPR00126; Bac_DNabinding; 1. BR FRIVES; PR00624; HISTONEHS.

BR PRNAT; SR00624; HISTONEHS.

BR SMART; SW0041; BHL; I. BR SW0041; BHL; I. BR SW041; BHL; I. SW041; BRCHERIAL HISTONE-LIKE DOMAIN.

101 214 DEGENERATE REPEATS REGION.

101 214 DEGENERATE REPEATS REGION.

Length 214;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
10NA-binding protein HU homolog (Histone-like protein) (Hlp).
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=H37Rv;
Prasad H.K., Annapurna P.S., Dey A.B., Tyagi J.S., Jain N.K.
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45.7%; Pred. No. 0.0021;
tive 4; Mismatches 28; Indels
                                                                                                                                                                                                                                     laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
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                                                                                                                                                                                                                                                                                                            [3]
SEQUENCE OF 71-86, AND DNA-BINDING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z83018; CABO5427.1; -.
EMBL; AE007127; AAK47393.1; -
HSSP; P02346; 1HUU.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D.
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nes 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DBH MYCSM
Q9ZHCS;
                                                                                                                                                                      Bishai W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DBH_MYCSM
AC Q92ZIC
DT 16-OC
DT 16-OC
DT 16-OC
DT 16-OC
DE DNA-D
GN HUP O
OS MYCOD
OC Bacte
OC Actin
OX (1)
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
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"The Drosophila hydei gene Dhmstlol(1) encodes a testis-specific,
"The Drosophila hydei gene Dhmstlol(1) encodes a testis-specific,
repetitive, axoneme-associated protein with differential abundance in
Y chromosomal deletion mutant files.";
Dev. Biol. 162:414-425(1994).
-!- FUNCTION: POSSIBLE STRUCTURAR ROLE IN THE SPERM TAIL. IT IS
ASSOCIATED WITH AXONEMAL STRUCTURES.
-!- SUBCELLULAR LOCATION: CYCOPIAGMIC (By similarity).
-!- TISSUE SPECIFICITY: TESTIS. LOCATED IN SPERMATOCYTES AND
                                                                                                                        111 AKKAAKKAPAKKAAAKKTATKAAAKKAPAKKAATKAPAKKAATKAPAKKAATKAPAKK-- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MST101(1).
Drosophila hydei (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKK---EKAYAKK--AEKAAKKAEAK--AYKAAEAKKKAKAEAKKYAKAAKAEKKE 53
                                                             Lee B.H., Murugasu-Oei B., Dick T.; "Upregulation of a histone-like protein in dormant Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.2%; Score 129; DB 1; Length 208; 52.4%; Pred. No. 0.0023; Live 6; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACTERIAL HISTONE-LIKE DOMAIN.
DEGENERATE REPEATS REGION.
CASFS77F61F7EF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Axoneme-associated protein mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF068138; AAD13809.1; -.
HSSP; PO2346; 1HUU.
InterPro; IPR000119; Bac DNAbind.
Pfam; PF00216; Bac DNA bInding; 1.
Probom; PD000945; Bac DNAbind; 1.
SMART; SM0041; BHL; 1.
STRAIN=ATCC 700084 / mc(2)155;
MEDLINE=99110209; PubMed=9894918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 -AATKAPAKKAAAKAPAKKAATKA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94200512; PubMed=8150205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 YAAAEAKYKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 208 AA; 21230 MW;
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ProDom; PD000373; Linkerhist_N; 1.
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P15869;
                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                       Matches
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                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                            19 X 16 AA APPROXIMATE TANDEM REPEATS OF K-K-C-X-E-X-A-[KQ]-K-X-X-E-X-A-X. 24C65D2510387E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                          81 AKK--EKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEK 138
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAKKAEKAAKKAE--AKAYKAAEAKKKAK--AEAKKYAKAKKE----- 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87172742; PubMed=3031476; Median 27., Median 27., Land 27., Land 27., Land 27., Land 27., Land Expression of the gene encoding tale histone subtype H1-gamma of the sea urchin Strongylocentrotus
                 DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELLCAL. POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN STRAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: BELONGS TO THE HISTONE HI/HS FAMILY.
                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                         DB 1; Length 344;
                                                                                                                                                                                                                                                                                      Score 127.5; DB 1; Length 3 Pred. No. 0.0043; 6; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                139 KKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEA 176
                                                                                                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
12-ULL-1999 (Rel. 38, Last annotation update)
Histone H1-gamma, late.
                                                                                                                                                                                                                                                                                                                                                                                                      51 -----KKEYAAAEAKYKAEAAK----AAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 AA
                                                                                                                                                                                      PIR; S34153; S34153.
FlyBase; FBgn0011816; Dhyd\mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSEP; P02259; 1HST.
InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist N.
Pfam; PR00538; linker_histone; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell. Biol. 7:478-485(1987)
                                                                                                                                                                                                                 Sperm; Repeat; Multigene family
DOMAIN 58 337 19
                                                                                                                                                                                                                                                             344 AA; 37793 MW;
                                                                                                                                                                          EMBL; X73480; CAA51875.1; -.
                                                                                                                                                                                                                                                                                       34.8%;
46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M16033; AAA30059.1; -.
                                                                                                                                                                                                                                                                                                                  46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
  SPERMATID BUNDLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A26721; A26721.
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 purpuratus.";
Mol. Cell. Bio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H1G_STRPU
P07796;
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88246461; PubMed=2837660;

Lai Z.-C., Childs G.;

Lai Z.-C., Childs G.;

Lai Z.-C., Childs G.;

Lai Z.-C., Childs G.;

La gene encoding the late histone subtype H1-beta of the sea urchin Strongylocentrotus purpuratus.";

Mol. Cell. Biol. 8:1842-1844(1988).

-I-FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.

-I-SUBCELLULAR LOCATION: Nuclear.

-I-SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                          2 KKYAKKEKAYAKKAEK------AAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Gaps
Productive and Montal 1.

Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 211 AA; 22169 MW; 9F214581334BBE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAK------AAKAEK
                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211;
                                                                                                                              Length 217;
                                                                                             Score 127; DB +,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.3%; Score 125.5; DB 1; Length 49.4%; Pred. No. 0.0041; ive 6; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
115-UUL-1999 (Rel. 38, Last annotation update)
Historne Hi-beta, late embryonic.
                                                                                                            34.7%; Score 45.2%; Pred. No. 0.005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M20314; AAA30052.1; -.
PIR; A28100; A28100.
HSSP; P02259; 1HST.
INTERPRO; IPR001386; Histone H1/H5.
INTERPRO; IPR003216; Linkerhist_N.
Pfan; PF00589; linker histone; 1.
ProDom; P0000373; Linkerhist_N.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                           185 РАККАААКРАККААКРАККААКРА 208
                                                                                                                                                                                                                                                                                                                                                         50 EKKEYAAAEAKYKAEAAKAAKEA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYAAAEAKYKAEAAKAAAKEAA 74
                                                                                                                                                     Local Similarity 45.2
nes 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strongylocentrotus.
NCBI_TaxID=7668;
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MEDLINE=80156832; PubMed=7363905;
Strickland W.N., Strickland M., Brandt W.F., von Holt C., Lehmann A.,
Mitmann-liabold B.;
Wittmann-liabold B.;
Wittmann-liabold B.;
Wittmann-liabold B.;
Wittmann-liabold B.;
With primary structure of histone H1 from sperm of the sea urchin parechinus angulosus. 2. Sequence of the C-terminal CNBr peptide and the entire primary structure.";
Eur. J. Blochem. 104:567-578(1980).
C. -- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLESCOME CHAINS INTO HIGHER ORDER STRUCTURES.
C. -- FUNCTION: William INTOHER NUCLEAR.
C. -- SUBCELLULAR LOCATION: Nuclear.
C. -- SUBCELLULAR LOCATION: Nuclear.
C. -- SIMILARITY: BERLONGS TO THE HISTONE H1/H5 FAMILY.
RING A02586; HSURIP.
RING HSSP: PO2259; HHST.
RINGERPRO; IPR001386; Histone H1/H5.
RINGERPRO; IPR001386; Linkerhist N.
RINGERPRO; PR000373; Linkerhist N.
RING PFam, PF000373; Linkerhist N.
RING SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 AKAAAKRKAALAKKKAAAAKRKAAKKAKKPKKKAAKKAKKPAKKSPKKAKKPAKKSP
                                                                        "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 1. Chemical and enzymatic fragmentation of the protein and the sequence of amino acids in the four N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Aedes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYAKKAEKAAK-KAEAKAYKAAEAKKKAKAEAKKYA-KAAKAEKKEYAAAE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Gavino V.H., Fallon A.M.;

"Aedes mosquitoes tribosomal protein S6 cDNA.";

"Andess mosquitoes tribosomal protein S6 cDNA.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN CONTROLLING CELL GROWTH

AND PROLIFERATION THROUGH THE SELECTIVE TRANSLATION OF PARTICULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSES OF MRNA (By similarity).
-!- PTM: Ribosomal protein S6 is the major substrate of protein kinases in eukaryote ribosomes (By similarity).
-!- SIMILARITY: BELONGS TO THE S6E FAMILY OF RIBOSOMAL PROTEINS.
                    Strickland W.N., Strickland M., de Groot P.C., von Holt C., Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.6%; Score 123; DB 1; Length 24 48.7%; Pred. No. 0.0071; tive 9; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> R.
1B25B3F136541947 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
40S ribosomal protein S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mosquito)
                                                                                                                                                cyanogen bromide peptides.";
Eur. J. Biochem. 104:559-566(1980).
       MEDLINE=80156831; PubMed=6767609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 144 K
248 AA; 26387 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aedes aegypti (Yellowfever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 KKKKAKRSPKKAKKAA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 70., Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 AKYKAEAAKAAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                             SEQUENCE OF 80-248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RS6 AEDAE
Q9U761;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Gavino V.H., Fallon A.M.;
Gavino V.H., Fallon A.M.;
Naedes mosquitoes ribosomal protein S6 cDNA.";
Submitted (NAY-1999) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN CONTROLLING CELL GROWTH
AND PROLIPERATION THROUGH THE SELECTIVE TRANSLATION OF PARTICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 AKKVAKKEAKKEVKKVTEAAKKADAKAAKVEPKKADKKSADSGKKATAGDKK----E 309
                                                                                                                                                                                                                                                                                             Aedes albopictus (Forest day mosquito).
Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Nematocera,
Culicoidea, Aedes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKE-KAYAKKAEKAAKKAEAKAYKA-AEAKKKAKAEAKKYAKAAKAEKKEYAAAE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSES OF MRNA (By similarity).
PTW: Ribosomal protein 56 is the major substrate of protein kinases in eukaryote ribosomes (By similarity).
SIMILARITY: BELONGS TO THE S6E PAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 AA; 39619 MW; 669A5DA33F8BADD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.3%; Score 125.5; DB 1
50.0%; Pred. No. 0.0061;
iive 6; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-199 (Rel. 38, Last annotation update)
Patcore H1, gonadal.
Parechinus angulosus (Angulate sea urchin).
                                                                                                                                                                         (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR01377; Ribosomal_S6E. Pfam; PF01092; Ribosomal_S6e; I ProDom; PD003460; Ribosomal_S6e; I PROSITE; PS00578; RIBOSOMAL_S6E; I Ribosomal protein; Phosphorylation.
156 KP-AAKKAAKKPAAKKPAAKKAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF154066; AAF04789.1; -.
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310 KKVEKKAAPAAKKEA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 38; Conservative
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                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7160;
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                                                                                                                                                                            15-JUN-2002
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P0<u>2</u>256;
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Length 248;

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Search completed: March 10, 2003, 12:17:10 Job time : 18:5443 secs
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Luropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Volckaert G., Voet M., Robben J.;
"Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the right arm of chromosome VII from Saccharomyces cerevisiae carrying the MAL1 locus reveals 15 complete open reading frames, including Yeast 13:51-229(1997).

-i- FUNCTION: 2-DNA BINDING PROTEIN. COULD BE INVOLVED IN CHROMOSOME ORGANIZATION.
                                                                                                                                                                                                                                                                                                                                                     6 KKEKAYAKKAEKAAKK-AEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAA-----A 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZUO1 OR YGR285C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                               33.6%; Score 123; DB 1; Length 346; 45.5%; Pred. No. 0.0092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang S., Lockshin C., Herbert A., Winter E., Rich A.; "Zuotin, a putative Z-DNA binding protein in Saccharomyces
                                                                                                                                                                                                                                                                                                                   25; Indels
                                                                                                                                                                                          ProDom; PD003460; Ribosomal_S6E; 1.
PROSITE; PS00578; RIBOSOMAL_S6E; 1.
Ribosomal protein; Phosphorylation.
SEQUENCE 346 AA; 39365 MW; S9CPF7B22BDBDFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 AA
                                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 1-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear. SIMILARITY: CONTAINS 1 J DOMAIN.
                                                                                                                                       EMBL, AF154067; AAF04790.1; -. InterPro, IPR001377; Ribosomal S6E. Pfam; PF01092; Ribosomal S6e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=20B-12;
MEDLINE=93010971; PubMed=1396572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S288c / FY1679;
MEDLINE=97245295; PubMed=9090054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerevisiae.";
EMBO J. 11:3787-3796(1992),
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306 EKKVEKKAAPAVAKKEA 322
                                                                                                                                                                                                                                                                                                                                                                                                                        EAKYKAEAAKAAAKEAA 74
                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 35, Conserva
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P32527;
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ZUO1_YEAST
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                                                                                                                                                                                                                                                                               33.6%; Score 123; DB 1; Length 433; 46.2%; Pred. No. 0.011; tive 10; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                              2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEK-
                                                                                                                                                                                                       170 J-DOMAIN.
357 ALA/LYS-RICH.
49019 MW; 0AA76BC11D3C7DAB CRC64;
             EMBL; Z73070; CAA97317.1; -.
PIR; S25194; S25194.
RSP PO8622; 1BQZ.
SGD; S0003517; ZU01.
InterPro; IPR001623; DnaJ.N.
PRANT; SM00271; DnaJ; 1.
PROSITE; PS00636; DNAJ.1; 1.
PROSITE; PS50076; DNAJ.1; 1.
Chaperone; DNA-binding; Nuclear protein.
DOMAIN 306 357 ALA/LYS-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         58 EAKYKAEAAKAAAKEAAY 75
EMBL; X63612; CAA45156.1;
                                                                                                                                                                                                                                                                                                    Best Local Similarity 46.29
Matches 36; Conservative
                                                                                                                                                                                                                                                 433 AA;
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March 10, 2003, 12:15:01; Search time 40.7743 Seconds (without alignments) 389.109 Million cell updates/sec
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366
1 AKKYAKKEKAYAKKABKAAK......BAKYKABAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                        671580
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp bacteria:*
sp bucteria:*
sp fungi:*
sp human:*
sp mammal:*
sp mammal:*
sp organele:*
sp phage:*
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_plan: \*
sp\_rodent: \*
sp\_virus: \*
sp\_virus: \*
sp\_vortebrate: \*
sp\_rollassified: \*
sp\_virus: \*
sp\_varceriap: \*
sp\_archerap: \*

			Description	Q8x965 escherichia	Q8zqt6 salmonella	Q8z8c1 salmonella	Q937k4 erwinia chr	Q9wwx1 pseudomonas	Q9cm70 pasteurella	Q39576 chlamydomon	O61164 plasmodium	Q98kg7 rhizobium l	Q26947 trypanosoma	08zgz2 yersinia pe	Q8xvn7 ralstonia s	093946 candida alb	Q8t5c8 plasmodium	Q84528 paramecium	Q92a67 listeria in
SUMMARIES			ΩI	Q8X965	OSZOT6	Q8Z8C1	Q937K4	Q9WWX1	Q9CM70				Q26947			093946	QBT5C8	084528	Q92A67
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			Match Length DB	394	407	376	395	372	389	232	1701	1341	1128	388	200	212	1866	311	243
	ф	Query	Match	40.4	40.4	39.9	39.8	38.9	38.3	37.7	37.7	37.0	36.6	35.7	35.0	34.3	34.0	33.5	33.3
			Score	148	148	146	145.5	142.5	140	138	138	135.5	134	130.5	128	125.5	124.5	122.5	122
		Result	No.	1	7	٣	4	വ	9	7	ω	σ	10	11	12	13	14	15	16

17 122 33.3 755 10 Q9FP71 18 121.5 33.2 239 16 Q8FSW4 19 120.5 32.9 284 065794 22 118.5 32.4 191 5 046142 22 118.5 32.4 191 5 046143 22 118.5 32.4 191 5 046143 22 118.5 32.4 233 5 018319 24 117.5 32.4 233 5 018319 22 118.5 32.4 235 5 018319 22 118.5 32.4 275 5 001395 28 117.5 32.1 265 10 Q95M19 29 117.5 32.1 265 10 Q95M19 32 116 31.7 224 13 Q90ZD7 32 116 31.7 224 13 Q90ZD7 33 115.5 31.6 191 5 Q8TSQ8 34 115.5 31.6 485 10 Q95MU5 31 114 31.1 591 6 Q95MU5 42 113.5 31.0 Q95MU5 42 113.5 31.0 Q95MU5 42 113.5 31.0 Q95MU5 44 113.5 31.0 Q95MU5 44 113.5 31.0 Q95MU5 5 Q95MU5 5 113.5 31.0 Q95MU5 5 Q95MU5 5 113.5 31.0 Q95MU5 5 Q95MU5 5 L13.5 31.0 Q95MU5	O9fp71 oryza sativ O895w4 listeria mo O65794 triticum ae O46142 mytilus edu O46143 mytilus edu O46143 mytilus edu O46362 mytilus edu O46362 mytilus edu O46362 mytilus edu O98319 chironomus O018319 chironomus O018319 chironomus O018596 chlamydomon O65795 triticum ae O9961 homo sapien O8559 plasmodium	Q8t9r3 leishmania O46140 mytlius edu Q23784 chirconeus Q8rxd0 arabidopsis Q9su08 arabidopsis Q26907 trypanosoma Q9h8h4 homo sapien Q9swu2 triticum ae Q9ru45 deinococcus Q9v6s7 drosophila Q9y168 plasmodium Q9swu3 triticum ae
122 33.3 120.5 33.3 119.5 33.2 118.5 32.4 118.5 32.4 118.5 32.4 118.5 32.4 117.5 32.1 117.5 32.1 116.5 31.0 115.5 31.6 115.5 31.6 115.5 31.6 115.5 31.6 115.5 31.6 115.1 31.1 114 31.1 113.5 31.0	011 010 010 010 011 013	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

# ALIGNMENTS

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MEDLINE=21534947; PubMed=11677608;
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                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 376 AA;
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                                  SEQUENCE FROM N.A.
             NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=556;
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  Salmonella
                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                    138 AAKAAADAKAKAEADDKAAEEAAKKAAADAKKKAEAEAAKAAAEAQKKAEAAAAALKKKA 197
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                        1 AKKYAKKEKAYA----KKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAA----KA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAEAKKYAKAAKAEKK-----EY 54
                                                                                                                                                                                                                                                                                                               Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.4%; Score 148; DB 16; Length 407; 54.4%; Pred. No. 0.00017; ive 8; Mismatches 13; Indels 20
                                                           Length 394;
                                                                                 21; Indels
                                    5B58D8E8230BDE28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   407 AA; 41865 MW; 2534352116602D75 CRC64;
                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                         40.4%; Score 148; DB 16;
55.1%; Pred. No. 0.00017;
iive 7; Mismatches 21;
                                                                                                                                                                                                                                   407 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 AAAEAKKKADAAAKAAADAKKKAAAEKAA 274
                                                                                                                                                                                                                                                                                         Tol protein, membrane spanning protein.
TOLA OR STM0747.
                                                                                                                                                                 55 AAAEAKYKAEAA-----KAAAKEAA 74
                                                                                                                                                    50 EKKEYAAAEAKYKAEAAKAAA-KEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                   PRT;
InterPro; IPR000104; Antifreeze_1.
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InterPro; IPR000104; Antifreeze 1.
PRINTS; PR00308; ANTIFREEZEI.
                                  394 AA; 40517 MW;
            PRINTS; PR00308; ANTIFREEZEI. Complete proteome.
                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
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20,
21,
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                                                 Ouery Match
Best Local Similarity 55.1%
....hes 49; Conservative
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 407 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tola protein.
STY0793.
                                    SEQUENCE
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Bascham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica servora Typhi (T18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pectobacterium.
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Ray M.C., Vianney A., Cotte-pattat N., Lazzaroni J.;
"characterization of the Erwinia chrysanthemi tol-pal genes.";
Submitted (CC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ297885; CAC82708.1; -.
SEQUENCE 395 AA; 41601 MW; 3COCIDC12E181013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 395;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        376 AA; 38804 MW; EC21F2C4767A8A42 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.9%; Score 146; DB 16;
54.4%; Pred. No. 0.00023;
iive 7; Mismatches 14;
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                                                                                                                                                                                                                                                                          Nature 413:848-852(2001).
EMBL; AL627268; CAD05209.1; -.
Interpro; IPR000104; Antifreeze.1.
PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01574; TUBBYPROTEIN.
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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DAAKKAEAA-AAAKKAA 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Conservative
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Q9WWX1

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May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL, AE006136; AAK03052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   061164;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Erythrocyte binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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49.4%; Pred. No. 0.00061;
ative 4; Mismatches 28;
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                                                                                                                                                                                                                                                                                                           51 ----KKEYAAAEAKYKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist N.
Pfam; PF00538; linker histone; I.
ProDom; PD000373; Linkerhist N; I.
                                                             HSSP, P19934; 170L.
InterPro; IPR000533; Tropomyosin.
PRNING; PR0194; TROPOMYOSIN.
Complete proteome.
SEQUENCE 389 AA; 42197 MW; B4(
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Best Local Similarity
Matches 41; Conserv
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01-MAR-2002
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SEQUENCE
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061164
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Q39576
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148 AKKAAEKQQADIAKKKAEDEAKKKAEEEAKKAAAEEAKKKAAEDAKKKAAEED 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rodriguez-Herva J.J., Ramos J.,
"Characterization of an OprL null mutant of Pseudomonas putida.";
"Dacterization of an OprL null mutant of Pseudomonas putida.";
Bacteriol. 178:5836-5840(1996).
EMBL; X74218; CAB50780.1;
InterPro; IPR001386; Histone—HI/HS.
PRINTS; PR00624; HISTONEHS.
                                                                                                                                                                                                                                                                     Rodriguez-Herva J.J., Ramos-González M.I., Ramos J.; "The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of cell envelope."; Bacteriol. 178:1699-1706(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pasteuralla multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MT-2;
Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
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46.9%; Pred. No. 0.00043;
iive 10; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 AKKKAAAEDAKKKAAEEAKKKAAADAOKKKAGEAARKA 245
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                 372 AA.
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                                                    Created)
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MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                   MEDLINE=96198174; PubMed=8626299;
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                                             01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20, TolA protein.
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                 PRELIMINARY;
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Submitted (JUN-1995)
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Best Local Similarity
                                                                                                                                    Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                    Pseudomonas.
NCBI_TaxID=303;
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                                                                                                                                                                                                                     SEQUENCE
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                 Q9WWX1
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Q9CM70
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103 AKKAATPKKAAAPKKEGAVKKTKAPKKEGEKKPKSAKKABKKPKKEGEKKKAAKPAKPAKAEK 162
                                                                                                                                       14; Gaps
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                                                                                                                                                                                                            1 AKKYA-----KKEKAYAKKAEKAAKKAE-AKAYKAAEA---KKKAKAEAKKYAKAAKAE- 50
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Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDIJINE=96120862; PubMed=8590479;
Fabry S., Mullar K., Lindauer A., Park P.B., Cornelius T., Schm
"The organization structure and regulatory elements of Chlamydo
histone genes reveal features linking plant and animal genes.";
Curr. Genet. 28:333-345(1995).
EMBL; U16725; AAA98452.1; --.
HSSP; P02259; 1HST.
                                                                 Query Match 38.3%; Score 140; DB 16; Length 389; Best Local Similarity 50.5%; Pred. No. 0.0007; Matches 46; Conservative 10; Mismatches 21; Indels 14
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389 AA; 42197 MW; B4032F2A2FD9E94B CRC64;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=SYLVIO X-10;

MEDLINE=93165082; bubbed=8381919;

Otsu K., Donelson J.E., Kirchhoff L.V.;

"Interruption of a Trypanosoma cruzi gene encoding a protein containing 14-amino acid repeats by targeted insertion of the neomycin phosphotransferase gene.";

Mol. Biochem. Parasitol. 57:317-330(1993).

EMBL; L04603; AAA96494.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAK-AEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004089; Chmtaxis transd.
InterPro; IPR001230; Prenyl site.
PROSITE; PS00294; PRENYLATION; UNKNOWN 1.
SEQUENCE 1128 AA; 119686 MW; 7997745D32B83656 CRC64;
                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Match 36.6%; Score 134; DB 5; Local Similarity 52.0%; Pred. No. 0.0059; nes 39; Conservative 9; Mismatches 23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 KYKAEAAKAAAKEAA
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                                                                                                                   Trypanosoma cruzi.
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                                                                                             R27-2 protein.
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Q8ZGZ2;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAYAKKAEKAAK------KAEAKAYKAAEAKKKAKAEAKKYAKA--- 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                 Kappe S.H.I., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.;
"A family of chimeric erythrocyte binding proteins of malaria parasites.",
Proc. Natl. Acad. Sci. U.S.A. 95:1230-1235(1998).
SEQUENCE 1701 AA; 199268 MW; EDA8E2DEFD87CE9A CRC64;
                                                                                                                                                                                                                                                                                                                                                      37.7%; Score 138; DB 5; Length 1701; 54.4%; Pred. No. 0.0043; Live 8; Mismatches 16; Indels 1;
                                              Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
10-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein ml11482.
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EMBL, AP002997; BAB48847.11, -.
Hypothetical protein; Complete proteome.
SEQUENCE 1341 AA, 138670 NW, 79C5DB1
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MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                  MEDLINE=98115903; PubMed=9448314;
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                                                                                                                                                                                                                                                                                                                                                                                                          43; Conservative
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Matches 43; Conservative
                   Plasmodium yoelii yoelii
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                                                                                                                   SEQUENCE FROM N.A.
                                                                  NCBI_TaxID=73239;
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Length 1128;

23; Indels

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STRAIN=CO-92 / BIOVAR ORIENTALIS;

MEDLINE=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Parkhill J., Wren B.W., Thomson N.R., Churcher C., Mungall K.L.,

Prentice M.B., Sebainia M., James K.D., Churcher C., Mungall K.L.,

Paker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Feltwell T., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stewens K., Whitehead S., Barrell B.G.,

"Genome sequence of Yersinia pestis, the causative agent of plague.";
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                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
388 AA
                                                                                                                                                                                                TolA colicin import membrane protein.
TOLA OR YPO1123.
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InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
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EMBL; AJ006637; CAA07165.1; -. NON TER 1 1 SEQUENCE 212 AA; 24231 MW;
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110 KKAEEEARKKA 120
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Q84528;
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MAEBL.
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Q84528
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Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
A Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Meissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
In "Genome sequence of the plant pathogen Ralstonia solanacearum.";
In "Genome sequence of the plant pathogen Ralstonia solanacearum.";
In "Genome sequence of the plant pathogen Ralstonia solanacearum.";
In "Genome sequence of the plant pathogen Ralstonia solanacearum.";
In "Genome sequence of the plant pathogen Ralstonia solanacearum.";
In "Genome sequence of the plant pathogen Ralstonia solanacearum.";
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In "Genome sequence of the plant pathogen Ralstonia solanacearum.";
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In "Genome sequence of the plant pathogen Ralstonia solanacearum.";
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In "Genome sequence of the plant pathogen Ralstonia solanacearum.";
In "Genome sequence" of the plant pathogen Ralstonia solanacearum.";
In "Genome sequence" of the plant pathogen Ralstonia solanacearum.";
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In "Genome Ralstonia solanacearum.";

Gaps
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Kaiser B., Kunkel W., Saluz H.P., Munder T.,

"Identification of Candida albicans protein domains with
transcriptional activating properties in Saccharomyces cerevisiae.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKA--KAEAKKYAKAAKAE 50
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Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
MCBI_TaxID=5476;
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                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
Probable histone H1 protein.
RSC2793 OR RSS0453.
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 AA; 19279 MW; D3831B590510272D CRC64;
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MEDLINE=21681879; Pubmed=11823852;
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214 VEVAEKAAADAA 225
                                                                                          63 AEAAKAAAKEAA 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
NCBI_TaxID=10506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Michon P., Stevens J.R., Kaneko O., Adams J.H.;
"Evolutionary relationships of conserved cysteine-rich motifs in adhesive molecules of malaria parasites.";
Mol. Biol. Evol. 0:0-0(2002).
EMBL; AX042083; AAL10508.1; -.
SEQUENCE 1866 AA; 212420 MW; DC692D7CFAE7D93F CRC64;
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                                             Score 125.5; DB 3; Length 212;
Pred. No. 0.0054;
9; Mismatches 27; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium vivax.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5855;
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212 AA; 24231 MW; 10C2122E9554A387 CRC64;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.0%; Score 124.5; DB 5;
50.0%; Pred. No. 0.054;
tive 10; Mismatches 23;
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(TrEMBLrel. 21, I
(TrEMBLrel. 21, I
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Matches 42; Conservative
                                                                    Local Similarity 47.9
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SEQUENCE FROM N.A.
MEDLINE=20478054; PubMed=11021991;
Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
"Characterization of a beta-1,3-glucanase encoded by chlorella virus
MEDLINE=20013326; PubMed=10544099; Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W., Lisec A.D., Nickerson K.W., Van Etten J.L.; "Chlorella virus PBCV-1 encodes a functional homospermidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.5%; Score 122.5; DB 12; Length 311; Best Local Similarity 48.6%; Pred. No. 0.013; Matches 36; Conservative 9; Mismatches 26; Indels 3;
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SEQUENCE FROM N.A.
Van Etten J.L.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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Graves M.V., Van Etten J.L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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Graves M.V., Van Etten J.L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gurnon J.R., Graves M.V., Van Etten J.L.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; U42580; AAC96576.1; -.
InterPro; IPR002048; BF-hand.
PROSITE; PS000189; BF-hand.
SEQUENCE 311 AA; 35390 MW; 9780E9582AFEF88A CRC64;
                                                                                                                                                                                                                                                    Van Etten J.L.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
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Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                  Virology 263:254-262(1999)
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126 EKAPAREAAKAAK 139

Search completed: March 10, 2003, 12:25:57 Job time: 41.7743 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model	March 10, 2003, 12:15:01; Search time 40.1245 Seconds (without alignments) 255.712 Million cell updates/sec	
OM protein -	Run on:	

US-09-816-989A-5 **BLOSUM62** Perfect score: Scoring table: Sequence:

908470 segs, 133250620 residues Gapop 10.0 , Gapext 0.5 Searched:

908470 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

/SIDS2/gcgdata/geneseq/geneseqp-embl /SIDS2/gcgdata/geneseq/geneseqp A\_Geneseq\_101002: .: /SIDS2/gcgdata Database

| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Copolymer molecula	Peptide #10 used i	Amino acid polymer	Poly-Lys-Ala used	Nucleic acid trans	Recombinant copoly				
SUMMARIES			ID	AAY82575	AAY82576	AAY82577	AAY82574	AAY82573	AAY98499	AAY59044	AAU04289	AAB45852	AAR06445
			DB	21	21	21	21	21	21	21	22	22	11
			Match Length DB	77	86	109	99	26	100	100	100	100	154
	ф	Query	Match	100.0	96.0	79.0	77.2	67.1	39.5	39.5	39.5	39.5	38.9
			Score	366	351.5	289	282.5	245.5	144.5	144.5	144.5	144.5	142.5
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	22 ABG28693 23 AAU09945 23 AAE13237 17 AAW06513 20 AAY32848 20 AAY23306
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# ALIGNMENTS

glatiramer accate, autoimmune disease, antiarthritic, neuroprotective, osteopathic; immunosuppressive, antithyroid; antiinflammatory; antidabetic; thyromimetic, haemostatic; antipsoriatic; dermatological; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5. Copolymer; molecular weight marker; TV-marker; immune disease; AAY82575 standard; peptide; 77 AA 28-JUL-2000 (first entry) AAY82575; AAY82575 

Unidentified

WO200018794-A1

06-APR-2000.

98US-0101693. 99WO-US22402. 24-SEP-1999; 25-SEP-1998;

(YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

06-APR-2000.

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glather acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or mutibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune baemolytic purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Gillain-Barre's syndrome, Hashimoco's disease, dilaparhic myxoedema, myasthenia gravis, psyndrome, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-seind disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to milecular weights molecules, which makes them ideal for use as
                                                                                                                                      Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                          Claim 10; Page 14; 72pp; English
                                                                                 WPI; 2000-317499/27.
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.; 0 Length 77; Indels 100.0%; Score 366; DB 21; 100.0%; Pred. No. 3.2e-27; ive 0; Mismatches 0; Local Similarity 100. nes 77; Conservative Query Match Matches

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61 YKAEAAKAAAKEAAYEA 77

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AAY82576 standard; peptide; 86 AA. 

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6

(first entry)

28-JUL-2000

Copolymer; molecular weight marker; TV-marker; immune disease; glatiframer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; hemostatic; antipsoriatic; dermatological; antiannaemic; immunosuppressive; demyelinating disease; osteopathritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; condition; multiple sclerosis; rheumatoid arthritis; condition; multiple sclerosis; rheumatoid arthritis; choin's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis;

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

AAY82577 standard, peptide; 109 AA.

AAY82577

28-JUL-2000 (first entry)

AAY82577;

Copolymer; molecular weight marker; TV-marker; immune disease;

. WO200018794-A1.

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides (I) for determining the molecular invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight cand an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related terrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple concertaintis, autoimmune bacenlytic anaemia, autoimmune cophoritis, outcoimmune thrombocytopaenia uveoretinitis, contact sensitivity disease, diabetes mellitus, Graves (Durbura, Colitis, contact sensitivity disease, diabetes mellitus, Graves (Inpus erythematosus. Mediated-mediated diseases which can be treated concertained molecular wishes psoriasis, peophigus vulgaris, or systemic include host-versus-staft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to malecular weights and prised them ideal for use as
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89.5%; Pred. No. 8.1e-26;
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                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 14; 72pp; English.
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(TEVA-) TEVA PHARM USA
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                                                             24-SEP-1999;
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28-JUL-2000 (first entry)

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of an an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune altibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic unamenia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune cureoretinits, contact sensitivity disease, diabetes mellitus, Graves diseases, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, poempligus vulgaris, or systemic lugars, erythematosus. Mediated-mediated diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated in the contact sensitivity diseases which can be treated to the companies of the contac
                                                Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mallituris, Graves disease; Gulliain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
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inflammatory condition; multiple sclerosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 14; 72pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US22402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-SEP-1999;
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                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2000.
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$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac
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                                                  32;
    Score 289; DB 21; Length 109;
Pred. No. 6.5e-20;
1; Mismatches 3; Indels 33
                                                                                                                                                                                                          61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAYKAEAKAAKEAAYEA 109
                                                                                                                                                                                   -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA
                                                                                            1 AKKYAKK-EKAYAKKA-----EKAAKKAEAKAYKAAEAKKKA
                                                                                                                                                                                                                                                                                                                                         AAY82574 standard; peptide; 66 AA
Query Match 79.0%;
Best Local Similarity 67.0%;
Matches 73; Conservative 1
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AAY82574 ID AAY8 XX AC AAY8 XX

RESULT 4

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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer acctate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-ediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic unecentaits, Crohn's disease, inclument thyroiditis, autoimmune uveoretinitis, Crohn's disease, chonic immune thyroiditis, autoimmune uveoretinitis, crohn's disease, chonic immune thyroiditis, autoimmune purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriaais, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                         glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyrominetic; haemostatic; antibaoriatic; dermatory; antidabetic; thyrominetic; haemostatic; antipaoriatic; dermatory; antianaemic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                               Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKEKAYAK----AKKAEAK-----AAKKAKAEAKKYAKAAKAEKKEYAAAEAK 49
                                                                                          Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
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Best Local Similarity 84.49
Matches 65; Conservative
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                                                                                                                                                                                                                                                                                                                                                               Unidentified
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21; Gaps

Indels

72.7%; Pred. No. 3.5e-16; ive 0; Mismatches 0;

56; Conservative

Matches

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Best Local Similarity

1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60

Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.

Peptide #10 used in nucleic acid transporter system.

(first entry)

31-JUL-2000

AAY98499;

AAY98499 standard; Peptide; 100 AA.

**AAY98499** 

50 YKAEAAKAAAKEAAYEA 66

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antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoria tribritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, duillain-Barre's syndrome, Hashimeto's disease, idiopachic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
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                                                                                                                                                                                                                                                                                                                                                                                   Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyvoid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidiamento; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Gulllain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                       Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.
                                                                            AAY82573 standard; peptide; 56 AA.
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                                        AAY 82873
AAY 82
RESULT 5
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(BAYU ) BAYLOR COLLEGE MEDICINE

93US-0167641. 92US-0855389 93WO-US02725

14-DEC-1993; 20-MAR-1992; 19-MAR-1993;

US6033884-A. 07-MAR-2000

Synthetic.

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The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA3631-A3652 and peptide sequences AAY98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver uncleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transgenic animals (as models or transforming cells or produce proteins, or transfecting cells in clude transforming cells to produce proteins, or transfecting cells in clude transforming cells to produce proteins, or transfecting cells in clude transforming cells to produce proteins, or transfecting cells in clude transfecting of felected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from endosomes, without requiring endosomal or lysosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent
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58.4%; Pred. No. 1.5e-06;
ive 6; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 125-128; 108pp; English.
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45; Conservative
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Best Local Similarity
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67.1%; Score 245.5; DB 21; Length 56;

Query Match

DB 21; Length 100;

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a "moiety that recognises and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is a capable of moving or initiating movement through a nuclear membrane; and/or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytosis, (c) a nucleus or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS can be used to treat disorders by targeting of specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells which allows the role of various nucleic acids to be studied by targeting expecific expression into specifically targeted tissue culture cells. The lysis agent within the NTS avoids the problem of endosomal/lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
3..100
/note= "Lys-Ala in positions 3 to 100 may be optionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                   1 AKKYAK-KEKAYAKKABKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                                                                                                                                                                                                                                                                                                                                           Nucleic acid transport system; NTS; cell surface receptor; cytosis; nuclear membrane; lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sparrow J,
                                                                                                                                                                                                                                                                                                                  Amino acid polymer seq ID NO: 64 of US5994109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Columns 123-124; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gottchalk S,
                                                                                                                                                                                                       AAY59044 standard; peptide; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0167641.
92US-0855389.
93WO-US02725.
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                                                                                                                                                                                                                                                                             (first entry)
                                                                                           62 AKAKAKAKAKAKAKA 78
                                                                         74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cristiano RJ,
                                                                       AKYKAEA-AKAAAKEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-038262/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1995;
                                                                                                                                                                                                                                                                               07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-DEC-1993;
20-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5994109-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                          AAY59044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WOO SLC,
                                                                                                                                                                  RESULT 7
                                                                                                                                                                                      AAY59044
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100 AA;

Sequence

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3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents poly-Lys-Ala, used to bind nucleic acid in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules is used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spacer molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Misc-difference 3..100
/note= "Lys-Ala in positions 3-100 may be present
absent"
                                                                                                                 1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sparrow J;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid transport; cytosis; ligand; lysis agent; gene therapy; hepatocyte; muscle; bone forming cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poly-Lys-Ala used in nucleic acid transporter system.
                     39.5%; Score 144.5; DB 21;
llarity 58.4%; Pred. No. 1.5e-06;
Conservative 6; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 131; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith LC, Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0167641.
92US-0855389.
93WO-US02725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
.....hes 45; Conserva
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6177554-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                              AAU04289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                  62
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RESULT 10
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                                                                                                          This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid. The nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor the transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems.
                                                                                                                                                                                                                                                                                                  Nucleic acid delivery, nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen; bacterial antigen.
Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                                                                                                                                                                                                                                                                  Nucleic acid transporter system peptide ligand SEQ ID NO 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WOO SLC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sottchalk S, Sparrow J, Cristiano RJ, Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 125-126; 105pp; English.
                                                                                                                                                            AAB45852 standard; Protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0167641.
92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0460971.
                                                                                                                                                                                                                                (first entry)
                                  AKYKAEA-AKAAAKEAA 74
                                                                   AKAKAKAKAKAKAKA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-049093/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 AA;
                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-1993;
20-MAR-1992;
                                                                                                                                                                                                                                21-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1993;
                                                                                                                                                                                             AAB45852;
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                                                                   62
                                  59
                                                                                                                                         AAB45852
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coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20.0VOY-1944 US.6459100), and plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences.

A methionine residue occurs between the Protein A and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences. C. the COP-1 polypeptide may be cleaved from the fusion protein. C. COP-1-77 contains oligonucleotide duplexes incoding the following segments: YKK, BEK, KAK, ARK, and AAA. The N-terminal alanine residue is left behind following CL rareage of the fusion protein. They are used to prevent, arrest or control a encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 KKYKKBAEEBEYKKKAKEAERAKKAKYKKKGAEAAKAAKAAAAAAAYKKEAEAAAEAEK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KKYAK--KEKAYAKKAEKA--AKKAEAKAY-KAAEAKKKAKAEA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 154;
                                                                                                                                                                                                                                        copolymer 1; COP-1-77; myelin basic protein; MBP; activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing genes encoding random polymers of aminoacid(s) - f
producing recombinant polypeptide(s) with biological and/or
                                                                                                                                                                               Recombinant copolymer 1-77, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.9%; Score 142.5; DB 1
43.4%; Pred. No. 3.7e-06;
iive 10; Mismatches 15
AAR06445 standard; protein; 154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 11, 25pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90US-0473845.
89US-0312541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90EP-0301700.
                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REPL-) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-255848/34.
                                                                                                                                                                                                                                                                                                      multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                See also AAQ05665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ05664.
                                                                                                                                                                                                                                                                       immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-1989;
                                                                                                                       03-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                          EP383620-A.
                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                           AAR06445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cook KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58 

59 AKYKAEA-AKAAAKEAA 74

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6; Mismatches

Conservative

45;

Matches

Local Similarity

Query Match

39.5%; Score 144.5; DB 22; Length 100; 58.4%; Pred. No. 1.5e-06;

80 KKAEKAKAAEKAKAAYK 96

RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coding for rCOP-1-19 were subcloned from pERV 2.1 to pBG3-2deltaN (deposit: 20-NOV.1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-19 contains oligonucleotide duplexes incoding the following segments: YKK, AAE, KAK, KKA, YEA, AKA KEA, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the supplements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control sdemyelinating disorder, e.g. multiple sclerosis. They may also de used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or
                                                                                                                                                                                                                        Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 38.3%; Score 140; DB 11; Length 106; Local Similarity 54.5%; Pred. No. 4.2e-06; Nes 42; Conservative 7; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    improve the expression of rCOP-1 polypeptides in E. coli,
                                                                                                                                                                                         Recombinant copolymer 1-19, myelin basic protein analogue.
72 AKYKKKAKEAEYKKKAKAAAAEAEYKKEAEEAEYKKYKKKAKKAKYK 117
                                                                                   AAR06446 standard; protein; 106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 12; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0473845.
                                                                                                                                                                                                                                                                                                                                                                                                   90EP-0301700
                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REPL-) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1990-255848/34.
N-PSDB; AAQ06446.
                                                                                                                                                                                                                                            immunological activ:
multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-1990;
                                                                                                                                                       03-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                    07-FEB-1990;
17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                               22-AUG-1990.
                                                                                                                                                                                                                                                                                                                               EP383620-A.
                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                     AAR06446;
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AAR84565-R84569 are polypeptides of the TCR27 protein of T.cruzi
The proteins are all fusion products with glutathione-5-transferase
(GST) and some contain a linker sequence. The TCR27 protein comprises
(GST) and some contain a linker sequence. The TCR27 protein comprises
(GST) and some contain a linker sequence. The TCR27 protein comprises
(CST) conserved 14 as sequence and a 68 as C-terminal region. This sequence
encodes the GST sequence, the Ag44 polypeptide contg. 16 of the 69
repeat units and also contains the amino and carboxy terminal
(CST) The TCR27 polypeptides of the invention are useful
for the diagnosis of Chagas disease (American Trypanosomiasis), they
are capable of detecting anti-T.cruzi antibodies; or for blood
screening. The TCR27 protein has epitopes to which most T.cruzi
infected individuals have antibodies. The TCR27 polypeptides with serum from patients with leishmaniasis, schistosomiasis,
or autoimmune disease and are hence less likely to cause false
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAK-AEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide(s) from the TCR27 protein of Trypanosoma cruzi - a
immunoassay reagent for specific diagnosis of Chagas disease, also
related nucleic acid and transformed cells
                                                                                                                                                                                                                                                                            /label= repeat region /note= "16 of \overline{6}9 repeat units of 14 amino acids"
                                                                                                                                                     TCR27; Chagas disease; repeat unit; diagnosis; blood screening; recombinant; fusion protein; glutathione-S-transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 36.6%; Score 134; DB 16; Length 643; Best Local Similarity 52.0%; Pred. No. 0.0001; Matches 39; Conservative 9; Mismatches 23; Indels 4
                                                                                                                     Trypanosoma cruzi TCR27 polypeptide, Ag15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 40-41; 68pp; English.
                                                                                                                                                                                                                                             Location/Qualifiers
              AAR84568 standard; Protein; 643 AA.
                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US03191.
                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Otsu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KIRC/) KIRCHHOFF L V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-344618/44.
N-PSDB; AAT05332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                643 AA;
                                                                                                                                                                                                           Trypanosoma cruzi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kirchhoff LV,
                                                                                                                                                                                                                                                                                                                                                                                                       20-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAR-1994;
                                                                                                                                                                                                                                                                                                                                   WO9525797-A1
                                                                                  09-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                      28-SEP-1995.
                                                 AAR84568;
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Region
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61 YKAEAAKAAAK-EAAYE 76

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32; Gaps

Indels

Pred. No. 1.1e-05;

50.6%;

Best Local Similarity 50.6 Matches 39; Conservative

0; Mismatches

547 TKVAEAEKQKAAEAA 561

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Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteogathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidiabetic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crown sisease; chronic immune thrombocytopeania purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre"s syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                               Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.
                       AAY82572 standard; peptide; 45 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                  99WO-US22402.
                                                                                                                                                                                                                                                                                                                                                          98US-0101693.
                                                                                                                                                                                                                                                                                                                                                                                (YEDA ) YEDA RES & DEV CO L'
(TEVA-) TEVA PHARM USA INC.
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                 WO200018794-A1
                                                                                                                                                                                                                                                                                                                                                                                                                      Lis D;
                                                                                                                                                                                                                                                                                                                                                          25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                  24-SEP-1999;
                                                                       28-JUL-2000
                                                                                                                                                                                                                                                                                                           06-APR-2000
                                               AAY82572
                                                                                                                                                                                                                                                                                                                                                                                                                     Gad A,
RESULT 13
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune CC diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple collerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic ansemia, autoimmune opphoritis, autoimmune thyroidists, autoimmune thoromocycopaenia uveoretinitis, contact sensitivity disease, diabetes mellitus, Graves purpura, collitis, contact sensitivity disease, diabetes mellitus, Graves disease, Glillain-Barre's syndrome, Hashimoto's disease, and collide host-versus-graft disease, and calayed-type hypersenatitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to collising an eacetare molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 AA
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35.8%; Score 131; DB 21; Length 45;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Mycobacterium DNA binding protein 1 immunogenic for pathogenic acid-fast bacteria for diagnosis, treatment and prevention of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 AKKVAK--KAPAKKATKAAKKAATKAPAKKAATKAPAKKAVKATKSPAKKVTKAVKKTAV 168
1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents the Mycobacterium bovis BCG strain mycobacterium DNA binding protein 1 (MDP1), which has immunogenicity against pathogenic acid-fast bacteria. The MDP1 protein can be used fidagnosis and treatment of diseases involving pathogenic acid-fast bacteria, such as tuberculosis, Mycobacterium avium intracellular complex (MAC) and Hansen's disease.
                                                                                                                                                                                                                                                                                        Mycobacterium bovis BCG strain; mycobacterium DNA binding protein 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAKKAEKAAKKA--EAKAYKAA-----EAKKKAKAEAKKYAKAAKAEKK 52
                                                                                                                                                                                                                                                                                                      MDP1; slow growing acid-fast bacterium protein; immunogenicity; pathogenic acid-fast bacterium; diagnosis; tuberculosis; MAC; Mycobacterium avium intracellular complex; Hansen's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.5%; Score 130; DB 21; Length 205; 49.4%; Pred. No. 7.2e-05; ive 7; Mismatches 26; Indels 10
                                                                                                                                                                                                                                                          Mycobacterium bovis BCG strain MDP1 protein SEQ ID NO:2.
                             1 AKKYAKK----AKAEKA-----KKAYKAAEAKKAAKYE----
                                                                                                                                                                AAB20575 standard; Protein; 205 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 2A; 62pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYAAAEAKYKAEAAKAAAKEAAYEA
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                                                                                                                                                                                                                            (first entry)
                                                                                        45
                                                           61 YKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Conservative
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                                                                                      30 -KAAAEKAAAKEAAYEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       such as tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-543393/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MATSUMOTO S.
                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium bovis
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                                                                                                                                                                                                                                                                                                                                                                                                WO200044905-A1
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                                                                                                                                                                                                                              08-DEC-2000
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                                                                                                                                                                                                AAB20575;
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(MATS/)
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ARR84565-R84569 are polypeptides of the TCR27 protein of T.cruzi

The proteins are all fusion products with glutathione-5-transferase
(GST) and some contain a linker sequence. The TCR27 protein comprises
(GST) and some contain a linker sequence. The TCR27 protein comprises

C a 95 amino acid (aa) N-terminal region; 69 repeats of a highly
C conserved 14 as sequence and a 68 as C-terminal region. This sequence
c conserved 14 as sequence and a 68 as C-terminal region. This sequence
c conserved units and also contains a linker sequence. The TCR27
polypeptides of the invention are useful for the diagnosis of Chagas
dissease (American Trypanosomiasis), they are capable of detecting
anti-T.cruzi antibodies; or for blood screening. The TCR27 protein
has epitopes to which most T.cruzi infected individuals have
antibodies. The TCR27 polypeptides will not react with serum from
c patients with leishmaniasis, schistcosomiasis, or autoimmune disease
and are hence less likely to cause false positives in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide(s) from the TCR27 protein of Trypanosoma cruzi - a immunoassay reagent for specific diagnosis of Chagas disease, also related nucleic acid and transformed cells
                                                                                                                                                                                                                                                                 Location/Qualifiers
241..450
/label= repeat_region
/note= "15 of 69 repeat units of 14 amino acids"
                                                                                                                                                                            TCR27; Chagas disease; repeat unit; diagnosis; blood screening; recombinant; fusion protein; glutathione-S-transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
35.5%; Score 130; DB 16; Length 472;
Best Local Similarity 51.4%; Pred. No. 0.00018;
Matches 38; Conservative 9; Mismatches 23; Indels
                                                                                                                                           Trypanosoma cruzi TCR27 polypeptide, Ag8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 44-45; 68pp; English
                                 AAR84569 standard; Protein; 472 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US03191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0216894
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KIRC/) KIRCHHOFF L V. (OTSU/) OTSU K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kirchhoff LV, Otsu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-344618/44.
N-PSDB; AAT05333.
                                                                                                                                                                                                                                   Trypanosoma cruzi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472 AA;
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                                                                                                                                                                                                                                                                                                                                                             WO9525797-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1995;
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                                                                                                       09-MAY-1996
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                                                                   AAR84569;
                                                                                                                                                                                                                                                                     Key
Region
RESULT 15
             AAR84569
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Gaps

360 ATKVAEAEK---QXAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEA 416

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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59

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Search completed: March 10, 2003, 12:21:30 Job time: 41.1245 secs
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GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
              Copyright
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- protein search, using sw model OM protein Run on:

March 10, 2003, 12:26:10 ; Search time 22.9051 Seconds (without alignments) 141.764 Million cell updates/sec

US-09-816-989A-5

Title: Perfect score:

1 AKKYAKKEKAYAKKAEKAAK......EAKYKAEAAKAAAKEAAYEA 77 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

188354 segs, 42170167 residues Searched:

Total number of hits satisfying chosen parameters:

188354

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published\_Applications\_AA:\* Database :

| Cgn2\_6/ptodata/1/pubpaa/USO8\_NEW\_PUB.pep:\*
| Cgn2\_6/ptodata/1/pubpaa/DGT\_NEW\_PUB.pep:\*
| Cgn2\_6/ptodata/1/pubpaa/DGT\_NEW\_PUB.pep:\*
| Cgn2\_6/ptodata/1/pubpaa/USO6\_NEW\_PUB.pep:\*
| Cgn2\_6/ptodata/1/pubpaa/USO7\_DUBGOMB.pep:\*
| Cgn2\_6/ptodata/1/pubpaa/USO7\_DUBGOMB.pep:\*
| Cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
1	366	100.0	77	10	US-09-816-989A-5	Sequence 5. Appli
7	351.5	96.0	86	10	US-09-816-989A-6	
е	289	79.0	109	10	US-09-816-989A-7	,
4	282.5	77.2	99	10	US-09-816-989A-4	4
Ŋ	245.5	67.1	26	10	US-09-816-989A-3	٠. س
y	141	38.5	372	σ	US-09-820-843A-8	. <
7	131	35.8	45	10	US-09-816-989A-2	
œ	124.5	34.0	452	σ	US-10-184-832-5	
σ	121	33.1	223	σ	US-10-051-643-201	
10	111.5	30.5	356	σ	US-09-820-843A-27	
11	104.5	28.6	35	10	US-09-816-989A-1	
12	104.5	28.6	309	σ	US-09-820-843A-24	4
13	104.5	28.6	617	10	US-09-864-761-36182	
14	102	27.9	369	6	US-09-820-843A-95	Sequence 95, Appl
15	66	27.0	102	σ	US-09-999-724-90	Sequence 90, Appl
16	66	27.0	218	σ	US-09-999-724-48	Sequence 48, Appl
17	66	27.0	434	10	US-09-124-280A-3	Sequence 3, Appli
18	98.5	26.9	892	10	US-09-815-242-13765	Sequence 13765, A
19	97.5	26.6	890	10	US-09-815-242-10314	Sequence 10314, A

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RESULT 2 US-09-816-989A-6 ; Sequence 6, Application US/09816989A

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Sequence 5197, Ap Sequence 5298, Ap Sequence 1294, A Sequence 100, App Sequence 46, Appl Sequence 11216, A Sequence 11216, A Sequence 1164, Ap Sequence 1184, Ap Sequence 18, Appl Sequence 18, Appli Sequence 9, Appli Sequence 8, Appli Sequence 9, Appli Sequence 11, Appli	Sequence 265, App Sequence 35829, A Sequence 16575, Ap Sequence 10575, Ap Sequence 4893, Ap Sequence 35241, A Sequence 7, Appli Sequence 2, Appli Sequence 599, App
9 US-09-738-626-5197 10 US-09-815-242-5298 10 US-09-815-242-12294 10 US-09-919-497-100 9 US-09-929-724-46 10 US-09-810-813-23 10 US-09-810-813-23 10 US-09-815-242-11216 10 US-09-815-242-11216 10 US-09-815-242-5198 10 US-09-815-242-5198 10 US-09-982-59 10 US-09-982-59 10 US-09-983-69-8 10 US-09-983-80-8 10 US-09-983-80-8 10 US-09-983-811	9 US-10-114-170-265 10 US-09-864-71-35829 9 US-09-864-71-85829 10 US-09-815-242-10575 10 US-09-815-242-4893 10 US-09-864-761-35241 9 US-10-093-892-7 10 US-09-923-304-2 10 US-09-923-304-2
600 454 454 454 454 382 300 829 840 840 840 840 840 840 840 840 840 840	519 88 365 769 782 89 220 265
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# ALIGNMENTS

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APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: CODOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1999-09-24
SOFTWARE: 1999-09-24
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
LENGTH...
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 366; DB 10; Best Local Similarity 100.0%; Pred. No. 6e-26; Matches 77; Conservative 0; Mismatches 0;
                 Sequence 5, Application US/09816989A Patent No. US20020115103A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
US-09-816-989A-5
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKETITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKETILE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09816989A

Batent No. US20020115103A1

GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doxis
TILLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKEITILE OF INVENTION: AND FOR THERAPEUTIC USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 77.2%; Score 282.5; DB 10; Length 66; 1 Similarity 84.4%; Pred. No. 9.6e-19; 65; Conservative 0; Mismatches 1; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
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SOFWARE: Patentin version 3.1
SEQ 1D NO LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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SEQ ID NO 3
LENGTH: 56
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                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gad, Alexander
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Best Local Similarity
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Best Local Similarity
Matches 65; Conserv:
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US-09-816-989A-3
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                                    APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERABEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: 05/101,693
PRIOR PLING DATE: 2998-09-25
PRIOR PLING DATE: 1998-09-25
PRIOR PLING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTHARE: PATCHIN VERSION 3.1
SEQ ID NO 6
LENGTH: 86
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APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
FILLE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 1998-09-25
PRIOR PILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 7
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAKAEKKEYAAAEAK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 351.5; DB 10; Length
Pred. No. 1.2e-24;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 289; DB 10;
Pred. No. 4.4e-19;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKK-EKAYAKKA-----EKAAKKAEAKAYKAAEAKKKA
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Patent No. US20020115103A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.0%; ; nilarity 89.5%; 1 Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 67.0%;
Matches 73; Conservative
US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Sequence 201, Application US/10051643

Publication No. US20020197265A1

Fubblication No. US20020197265A1

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L. J.

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: System using Mycobacterium Vaccae

FILE REFERENCE: 11000.1008c2

CURRENT APPLICATION NUMBER: US09/156,181

FRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1999-09-17

PRIOR FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 208

SEQ ID NO 201

LENGTH: 223
                                                                                                                                                                                                                                                                                        WS-10-184-832-5

1 Sequence 5, Application US/10184832

2 Sequence 5 Application US/10184832

3 Sequence 5. Application No. 1020030022857A1

3 GENDRAL INFORMATION:

4 APPLICANT: Xu et al.

5 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

7 TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

7 TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

7 TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

7 CURRENT APPLICATION NUMBER: 2002-06-28

7 FRIOR APPLICATION NUMBER: 60/303,250

7 PRIOR FILING DATE: 2001-07-05

7 NUMBER OF SEQ ID NOS: 6

7 SOFTWARE: FASELSEQ for Windows Version 4.0

7 SEQ ID NOS:
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                         1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 34.0%; Score 124.5; DB 9; Best Local Similarity 56.0%; Pred. No. 0.00041; Matches 42; Conservative 7; Mismatches 21;
                                                                                1 AKKYAKK----AKAEKA----KKAYKAAEAKKAAKYE--
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                                                                                                                                      61 YKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                       30 -KAAAEKAAKEAAYEA 45
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152 AKAEAKAEAKAEAKE 166
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US-10-184-832-5
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US-10-051-643-201
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Sequence 8, Application Wo. US20030039963A1

GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: USFUL AS ANTI-INFECTIVES
FILE REFERENCE: QS3915
CURRENT PILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature;
CTHER INFORMATION: outer membrane integrity protein (tolA);
NAME/KEY: misc_feature
CTHER INFORMATION: gi[1573353
US-09-820-843A-8
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Patent No. US20020115103A1

GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
ITLE OF INVENTION: COPOLYMER I RELATED POLYPEP'
ITLE OF INVENTION: AND FOR THERAPEUTIC USE
ILE REPERENCE: 2609/60807-A-PCT-US
CURRENT FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARER PATENT NOS: 7

SOFTWARER: PATENT NOS: 7

SOFTWARER: PATENT NOS: 7

SOFTWARER: PATENT NOS: 7

SOFTWARER: PATENT NOS: 7

SEQ ID NO 2

LENGTH: 45
1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK--
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ORGANISM: Artificial Sequence
                                                                                        40 YKAEAAKAAAKEAAYEA 56
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Best Local Similarity 50.6
Matches 39; Conservative
                                                      61 YKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: H. influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-09-816-989A-2
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Sequence 24, Application US/09820843A
Publication No. US20030039963A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANTION:
APPLICANTION:
ACMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-9584-761-56185 Application US/09864761

| Sequence 36182, Application US/09864761
| Patent No. US20020048763A1
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G. | APPLICANT: Hank, David R. | APPLICANT: Hank, David R. | APPLICANT: Hank, David R. | APPLICANT: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE OF INVENTION UNBER: US 60/180,312 | PRIOR APPLICATION NUMBER: US 60/180,312 | PRIOR PELLING DATE: 2000-02-04 | PRIOR FILING DATE: 2000-08-26 | PRIOR FILING DATE: 2000-08-08-03 | PRIOR FILING DATE: 2000-08-04 | PRIOR FILING DATE: 2000-08-27 | PRIOR FILING DATE: 2000-09-27 | PRIOR FILING DATE: 2000-09-27 | PRIOR FILING DATE: 2000-09-27 | PRIOR APPLICATION NUMBER: US CT/USO1/00666 | PRIOR APPLICATION NUMBER: PCT/USO1/00666 | PRIOR APPLICATION NUMBER: PCT/USO1/00667 | PRIOR PLING DATE: 2001-01-30
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                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
COGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: misc feature
COTHER INFORMATION: polyhydroxyalkanoate synthesis protein PhaF
NAME/KEY: misc feature
COTHER INFORMATION: gi|9951352
US-09-820-843A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 309;
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                             Indels
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1 Similarity 65.8%; Pred. No. 0.0016; 25; Conservative 4; Mismatches 6;
                                                                                                              40 AKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKEAAYEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 KEYAAAEAK--YKAEAAKAAAKEAAYEA 77
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-864-761-36182
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US-09-820-843A-24
                             Matches
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TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-81,6-989A-1
                               Gaps
1 AKKYAKKEKAYAKK--AEKAAKKAEAKAYKAAEAKKKAKAE----AKKYAKAAKAEKKEY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKKA-----EKAAKKAEAK--AYKAAEAK-KKAKAEAKKYAK---- 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 30.5%; Score 111.5; DB 9; Length 3: Best Local Similarity 40.7%; Pred. No. 0.0043; Matches 44; Conservative 13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 ------AAKAEK----KEYAAAEA-----KYKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: US/09/816,989A
PRIOR PILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
SEQ ID NO 3.5
                                                                                                                                                                                                                                                                                               Sequence 27, Application US/09820843A Publication No. US20030039963A1 GENERAL INFORMATION:
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Patent No. US20020115103A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
CTHER INFORMATION: tola protein
NAME/KEY: misc feature
OTHER INFORMATION: gi|9656364
US-09-820-843A-27
                                                                                                                                                            180 ATKAAPAK-KAPAKKAATKAA 199
                                                                                                        55 A--AAEAKYKAEAAKAAAKEA 73
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                                                                                                                                                                                                                                                                          US-09-820-843A-27
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8 EKAYAKKAEKAAKK - - AEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEA 65
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                                                                                                                                                                                            9
                                                                                                                            Query Match 27.9%; Score 102; DB 9; Length 369; Best Local Similarity 43.1%; Pred. No. 0.03; Matches 31; Conservative 16; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KOVESDI, INRE
APPLICANT: BROUGH, DOUGLAS E.
TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
FILE REFERENCE: 212960
CURRENT APPLICATION NUMBER: US/09/999,724
CURRENT FILING DATE: 2001-10-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-10-24
PRICR APPLICATION NUMBER: US 09/101/751
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 08/700,846
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1995-08-21
PRIOR FILING DATE: 1995-11-28
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PATENTING DATE: 1995-11-28
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PATENTING DATE: 1905-11-28
NUMBER OF SEQ ID NOS: 94
SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: March 10, 2003, 12:53:44 Job time : 24.0479 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 90, Application US/0999724
Publication No. US20030022355A1
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
; NAME/KEY: misc_feature
; OTHER INFORMATION: gi|3322751
US-09-820-843A-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : :|||| || || ||
64 AEEKRAEAEAAAEAAPAA 82
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325 EEARRKEAEFEA 336
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Best Local Similarity
Matches 32; Conserv
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Sequence 95, Application US/09820843A
Sequence 95, Application US/09820843A
Sequence 95, Application US/09823A1
Sequence 95, Application OS US200003963A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REPRERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
SEQ ID NO 95
LENGTH: 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INPORMATION: MAP TO AC005529.7

OTHER INPORMATION: EXPRESSED IN HELA. SIGNAL = 1.3

OTHER INPORMATION: EXPRESSED IN HELALOO, SIGNAL = 0.94

OTHER INPORMATION: EXPRESSED IN HEART, SIGNAL = 1.3

OTHER INPORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.1

OTHER INPORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.3

OTHER INPORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.6

OTHER INPORMATION: SWISSPROT HIT: P12036, EVALUE 2.00e-33
                                                                             FRIOR APPLICATION NUMBER: FCT/USU1/USES)
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-03-0
FRIOR FILING DATE: 2001-01-03-0
FRIOR APPLICATION NUMBER: PCT/US01/00668
FRIOR APPLICATION NUMBER: PCT/US01/00663
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2000-09-21
FRIOR FILING DATE: 2000-09-21
FRIOR FILING DATE: 2000-06-30
FRIOR FILING DATE: 2000-06-30
FRIOR FILING DATE: 2000-06-30
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2000-06-30
FRIOR FILING DATE: 2000-06-30
FRIOR FILING DATE: 2001-01-30
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OTHER INFORMATION: conserved hypothetical protein
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170 KSPAEVKSPEKAKSPAKEEA 189
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ORGANISM: Homo sapiens
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FEATURE:
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LENGTH: 617
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US-08-460-890A-64
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Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 2, Appli
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                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 3
Sequence 1
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Sequence
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2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd
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US-08-167-641C-64
US-08-462-040A-64
US-08-162-040B-8
US-08-115-746-10
US-09-115-746-10
US-09-115-746-2
US-09-115-746-2
US-09-115-746-2
US-09-115-746-2
US-09-115-746-2
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US-09-115-746-2
US-09-115-746-2
US-09-115-746-3
US-09-11-889-3
US-09-041-889-3
US-09-041-889-3
US-09-041-889-3
US-08-929-414-1
US-08-929-414-1
US-08-929-414-1
US-08-939-674A-51
                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                            262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                              Issued Patents AA:*
                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                US-09-816-989A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433
223
223
223
56
1507
222
222
222
222
222
         Copyright
                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144.5
144.5
144.5
144.5
134
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119.5
119.5
1114
1110.5
110.5
110.5
110.5
1107.5
1107.5
1107.5
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123
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                                                                                                                                                           Sequence:
                                                                                                                                                                                                                            Searched:
                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
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, Appl	Sednence 52	US-08-993-674A-52	4	442	26.5	97	45
, Appl	Sequence 52	US-08-834-306-52	ო	442	26.5	97	44
i, Appl	Sequence 54	US-08-557-309B-54	N	219	26.8	98	43
Appli	Sequence 2,	US-09-344-529-2	4	92	56.9	98.5	42
Appl	Sequence 3,	US-08-456-112B-3	7	434	27.0	66	41
Appli	Sequence 3,	US-08-097-830E-3	Н	434	27.0	66	40
		US-09-101-751A-48	4	218	27.0	66	39
	Sednence 9(	US-09-101-751A-90	4	102	27.0	66	38
	Sequence 62	US-08-462-040-62	4	100	27.0	66	37
	Seguence 62	US-08-460-971A-62	4	100	27.0	66	36
	Sequence 62,	US-08-167-641C-62	ო	100	27.0	66	35
	Sequence 62	US-08-460-890A-62	N	100	27.0	66	34
	Sednence 38	US-09-041-889-38	ო	116	27.2	99.5	33
, Appl	Sequence 16	US-08-293-284A-16	N	9	27.7	101.5	32
	Sequence 16	US-08-346-849-16	Н	9	27.7	101.5	31
Appli	Sequence 4,	US-08-837-058-4	m	218	27.9	102	30
Appli	Sequence 4,	US-09-041-889-4	ო	218	27.9	102	29
Appli	Sequence 5,	US-08-993-008A-5	4	48	29.1	106.5	28

ALIGNMENTS

```
Sequence 64, Application US/08460890A

Patent No. 5994109

GENERAL INFORMATION:

APPLICANT: Woo, Savio L.C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gretchalk, Stephen
TITLE OF INVENTION: WUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: WUCLEIC ACID TRANSPORTER SYSTEMS STREET: 633 West Fifth Street
SYREET: Galiconia
COUNTRY: U.S. Angeles

COUNTRY: U.S. Angeles

STREET: Suice 4700
CITY: Los Angeles

CONFUTER: Day Angeles

CONFUTER: Day Angeles

CONFOUTER: Day Angeles

CONFOUTER: Unne S. 1995

CONFOUTER: Day Conformance

CONFOUTER: Unne S. 1995

CLASSIFICATION NUMBER: U.993

APPLICATION NUMBER: 07/855,389
FILING DATE: December 14, 1993

APPLICATION NUMBER: 07/855,389
FILING DATE: December 14, 1993

APPLICATION NUMBER: 32,327

RESERRICE/DOCKET NUMBER: 32,327

RESERRICE/DOCKET NUMBER: 32,327

FILING DATE: March 20, 1992

APPLICATION NUMBER: 32,327

FILING DATE: March 20, 1992

APPLICATION NUMBER: 32,327

FILING DATE: March 30, 1993

ATTORNEY AGBNT INFORMATION:

NAME: Warburg REALD ATTORNEY SEQ ID NO: 64:

FELERAK: (213) 489-1600

TELEFAK: (213) 489-1601

TELEFAK: (213) 489-1601

TELEFAK: (213) 489-1601

TELEFAK: (213) 489-1601

TELEFAK: (1219 55-0440

TELEFAK: (1219 55-0440

TELEFAK: FILE MAIN CALLES

LENGTH: 100 cmino acids

TTELEFAK: (1219 55-0440

TTELEFAK: (1219 55-0440

TTELEFAK: (1219 56-0440

TTELEFAK: (
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1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                                                                                                                                                                                                                                  Sequence 64, Application US/08460971A

Patent No. 6150168

GENERAL INPORMATION:
APPLICANT: Woo', Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gottchan, Richard J.
APPLICANT: Gottchank, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SUDURNESS: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                   Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.5%; Score 144.5; DB 4; Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-460-971A-64
                                                                                                                                Indels
                                                            39.5%; Score 144.5; DB 3; ilarity 58.4%; Pred. No. 2.7e-07; Conservative 6; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: ENGRAGE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM P.C. DOS 5.0
SOFTWARE: FASTER TOWNER: US/08/460, 971A
FILING DATE: US/08/460, 971A
APPLICATION NUMBER: 07/855, 389
FILING DATE: MARCH 19, 1993
APPLICATION NUMBER: 07/855, 389
FILING DATE: MARCH 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: MARDING NATHER COMPATIBLE
COMPUTER MARCH 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: MARDING NATHER COMPATIBLE
COMPUTER MARCH 10, 1993
ATTORNEY/AGENT INFORMATION:
NAME: MARDING NATHER COMPATIBLE
COMPUTER COMPUTER COMPATIBLE
COMPUTER COMPATIBLE
COMPUTER COMPUTER COMPUTER COMPATIBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPREDICATION NUMBER: 212/0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 64:
SEQUIENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 100 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                     59 AKYKAEA-AKAAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                            Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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   US-08-167-641C-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-460-971A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 64, Application US/08167641C
; Sequence 64, Application US/08167641C
; Patent No. 6033884
; GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Sailte 4700
; STREET: California
CCINY: Los Angeles
; CITY: Los Angeles
; CTTY: Los Angeles
; CTTY: Los Lyon
; US.A.
                                                                                                                                                                                                                           Query Match
39.5%; Score 144.5; DB 2; Length 100;
Best Local Similarity 58.4%; Pred. No. 2.7e-07;
Matches 45; Conservative 6; Mismatches 23; Indels 3
                                                                                       "Lys Ala" in positions 3 to 100 may be present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER PRADABLE PORM:
OFFWARE: FAALSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIFICATION NUMBER: US/08/167,641C
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 205/012
FILING DATE: March 19, 1993
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 205/012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH 100 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 AKYKAEA-AKAAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                 CTHER INFORMATION:
COTHER INFORMATION:
US-08-460-890A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
US-08-167-641C-64
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    1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Corsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.6%; Score 134; DB 2; Length 643; lilarity 52.0%; Pred. No. 1.8e-05; Conservative 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09115746

Patent No. 6228601

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Scephen A.
REGISTRATION NUMBER: 99,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                  US-08-216-894-8
; Sequence 8, Application US/08216894
; Patent No. 5876734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 643 amino acids
amino acid
                                                                                                                             62 AKAKAKAKAKAKA 78
                                                                                       59 AKYKAEA-AKAAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547 TKVAEAEKOKAAEAA 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 KYKAEAAKAAKEAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-216-894-8
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                                                                                                                                                                                              RESULT 5
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                          Gaps
                                                                1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                                                                                       3,
                                                                                                                                                                                                                                                                                     Sequence 64, Application US/08462040

Fatent No. 617554

GENERAL INFORMATION:

APPLICANT: Woo, Savio L.C.

APPLICANT: Smith, Louis C.

APPLICANT: Gettchalk, Stephen

TITLE OF INVENTION: NUCLEIC ACTIONS

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEB: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: California

COUTRY: U.S.A.

COUTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                        23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.5%; Score 144.5; DB 4;
58.4%; Pred. No. 2.7e-07;
iive 6; Mismatches 23;
58.4%; Pred. No. 2.7e-07; ive 6; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CALLIOGILIA
COUNTRY: CALLIOGILIA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION S36
PRICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/0893/02725
FILING DATE: March 19, 1993
ATTORNEY, AGENT INPORMATION:
NAME: WASHING INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212/078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEX: 67-350
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                          62 AKAKAKAKAKAKAKA 78
                                                                                                                                                   59 AKYKAEA-AKAAAKEAA 74
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 39.5
Best Local Similarity 58.4
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                 US-08-462-040-64
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360 ATKVAEAEK---QKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEA 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKKAEKAAKKAEAXAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59
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| Sequence 10, Application US/09115746
| Patent No. 6228601
| GENERAL INFORMATION:
| APPLICANT: Kirchhoff, Louis V. |
| TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION |
| TITLE OF INVENTION: WITH TRYPANOSOWA CRUZI |
| CORRESPONDECS: 10
| CORRESPONDECS: 10
| ADDRESSE: Foley & Landner |
| STREET: 3000 K Street, N.W., Suite 500 |
| CITY: Washington, D.C. |
| CONTAINED |
| CONTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.5%; Score 130; DB 2; Length 472; Best Local Similarity 51.4%; Pred. No. 3.1e-05; Matches 38; Conservative 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 472;
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51.4%; Pred. No. 3.1e-05;
tive 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: WEAD TO THE WASHINGTON, D.C.

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85326/102/DRLO
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REPERENCE/DOCKET NUMBER: 8532
TELECOMMUNICATION INFORMATION:
                             TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 472 amino acids
amino acid
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Best Local Similarity 51.4*
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-216-894-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 TKVAEAEKQKAAEA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 KYKAEAAKAAAKEA 73
                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08216894
; Patent No. 5876734
; GENERAL INFORMATION:
; APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
; TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; COTTY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.6%; Score 134; DB 4; Length 643; 52.0%; Pred. No. 1.8e-05; Live 9; Mismatches 23; Indels
                                                                                                                            ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIN Release #1.0, Version #1.25
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE POM:
COMPUTER READABLE FOM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFWMER: PACENTIN Release #1.0, Version #1.25
CURENT APPLICATION DARA:
APPLICATION NUMBER: US/08/216,894
FILIMG DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 85326/102/DRLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFLILIA.

PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5309
TELEFAX: (202)672-5399
                             STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 643 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.0°
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 547 TKVAEAEKOKAAEAA 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 KYKAEAAKAAKEAA 74
ADDRESSEE:
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                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-115-746-8
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Diagnosis, Prevention and Treatment of
Ulcerative Colitis, and Clinical Subtypes Thereof, Using
Microbial UC pANCA antigens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 564;
                                                                                                                     COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILLING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.5%; Score 130; DB 4;
51.4%; Pred. No. 3.7e-05;
tive 9; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REPERRENCE/DOCKET NUMBER: 85326/102/DRLO
         3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR PELICATION DATA:
APPLICATION NUMBER: US 08/837,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/09041889;
Patent No. 6033664
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer;
ITILE OF INVENTION: Diagnosis, Prev
TITLE OF INVENTION: Microbial UC pA
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  564 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 51.4<sup>§</sup>
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino acid
                                         Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-09-115-746-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505 TKVAEAEKQKAAEA 518
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CITY: San Diego
STATE: California
                                               COUNTRY: USA
COUNTRY: USA
TTA: 20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
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448 ATKVAEABK---QKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEK 504
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                                                                                                                                                                                                                                                                                           JOS-US-116-194-2.

Sequence 2, Application US/08216894

Patent No. 5876734

GENERAL INFORMATION:

APPLICANT: Kirchhoff, Louis V.

APPLICANT: Cotsu, Keiko

ITILE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION

TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 2007-5109

COMPUTER: READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER: PatentIn Release #1.0, Version #1.25

CURRET APPLICATION NUMBER: US/08/216,894

FILING DATE: 24-MAR-1994

ATTORNEY/AGENT INPORMATION:

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 29,768

RELECOMMUNICATION INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

TELLECOMMUNICATION INFORMATION:

TELLECOMMUNICATION INFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.5%; Score 130; DB 2; Length 564; Best Local Similarity 51.4%; Pred. No. 3.7e-05; Matches 38; Conservative 9; Mismatches 23; Indels
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Patent No. 6228601
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 564 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                        417 TKVAEAEKOKAAEA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    505 TKVAEAEKQKAAEA 518
                                                                                            60 KYKAEAAKAAKEA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 KYKAEAAKAAAKEA 73
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                                                                                                                                                                                                                                                                        US-08-216-894-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-216-894-2
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US-09-115-746-2
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-293-284A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-293-284A-2
                  US-08-346-849-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 129.5; DB 3; Length
Pred. No. 1.5e-05;
4; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIAIE: MASBACHUSELES

CUNNTRY: U.S.A.

ZIP: 02173-4799

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATCHIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/346,849

FLING DATE: CLASSIFER 1992

PRIOR APPLICATION NUMBER: 07/973,326

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/973,326

FLING DATE: 28 DECEMBER 1992

ATORNEY/AGENT INFORMATION:

NAME: BLOOK, David E.

REGISTRATION NUMBER: MIT-6008

FELERBHONE: (617) 861-6240

TELEBHONE: (617) 861-6240

TELEBHONE: (617) 861-9540

INPORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

MENGTH: 433 amino acids

TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zhang, Shuguang
APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Lockshin, Curtis
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES ITILE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC INUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 TKAVKKTAVKASVRKAATKAPAKKAAAKRPATKA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 AAA-----EAKYKAEAAKAAAKEAAYEA 77
                  ATTORNEY AGENT INPORMATION:
NAME: Campbell, Cathryn A.
REGISTAATION UNDHER: 31,815.
REPERRINGE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEFRONE: (619) 535-9001
TELEFRX: (619) 535-901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08346849
Patent No. 5670483
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.4%;
ilarity 45.7%;
Conservative
FILING DATE: 11-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: peptide
US-09-041-889-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-08-346-849-2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEK---KEYAAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: Diecreio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEB: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
  Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.6%; Score 123; DB 2; Length 433; 46.2%; Pred. No. 0.00013;
                                                      28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02.173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/293,284A
FLING DATE: 22-AUG-1994
CLASSIFICATION NUMBER: 07/973,326
RILNG APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FLING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
Query Match 33.6%; Score 123; DB 1; Best Local Similarity 46.2%; Pred. No. 0.00013; Matches 36; Conservative 10; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08293284A Patent No. 5955343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brook, David E.
REGISTRATION NUMBER: 22.592
REFERENCE/DOCKET NUMBER: MIT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (617) 861-6240
                                                                                                                                                                                                                                        350 AKKKNKRAIRNSAKEADY 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       58 EAKYKAEAAKAAAKEAAY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 EAKYKAEAAKAAAKEAAY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                              Sequence 201, Application US/09095855
Patent NO. 6160093
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
GITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKEKAYAKK--AEKAAKKAEAKAYKAABAKKKAKAE----AKKYAKAAKAEKKEY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.1%; Score 121; DB 4; Length 223; 55.6%; Pred. No. 9.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIPCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
APPLICATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 A--AAEAKYKAEAAKAAAKEA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
350 AKKKNKRAIRNSAKEADY 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 223 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 55.6
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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Sequence 201, Application US/09205426 Patent No. 6406704

RESULT 15 US-09-205-426-201

180 АТКААРАК-КАРАККААТКАА 199

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APPLICANT: Mateon, James D.

APPLICANT: Mateon, James D.

TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
FILE REPERRICE: 1996-12-04

CURRENT APPLICATION NUMBER: 08/095,855

EARLIER FILING DATE: 1997-12-23

EARLIER FILING DATE: 1997-12-23

EARLIER FILING DATE: 1997-12-23

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

protein search, using sw model OM protein Run on:

March 10, 2003, 12:15:04; Search time 25.2194 Seconds (without alignments) 327.825 Million cell updates/sec

US-09-816-989A-6 Title: Perfect score:

1 AKKYAKKEKAYAKKAEKAAK........KKAYKAEAAKAAAKEAAYEA 86 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ф			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	T I	Description
7	164	40.1	421	. 2	JV0057	tolA protein - Esc
0	157.5	38.5	376	~	AG0592	tolA protein (impo
m	156.5	38.3	1701	7	T09127	probable erythrocy
4	155	37.9	394	7	F90725	
ហ	155	37.9	394	N	G85576	membrane spanning
9	154	37.7	347	7	E83525	Tola protein PA097
7	151	36.9	210	8	A25550	histone H1 - sea u
œ	149	36.4	231	7	859589	histone H1 - Chlam
6	147.5	36.1	388	~	AC0138	
10	147	35.9	214	N	G70673	probable hupB - My
11	144	35.2	211	N	A28100	
12	142.5	34.8	344	~	834153	mst101-1 protein -
13	142	34.7	372	~	G64064	outer membrane int
14	140.5	34.4	328	04	A44993	cytosolic repetiti
15	140.5	34.4	1390	~	S51364	sperm tail-specifi
16	138	33.7	217	7	A26721	histone H1-gamma,
17	137.5	33.6	1128	N	T30296	R27-2 protein - Tr
18	135	33.0	219	~	E60110	repetitive protein
19	134	32.8	206	~	809388	histone H1 - sea u
20	133.5	32.6	384	~	B43592	outer membrane pro
21	133.5	32.6	433	7	S25194	Š
22	132.5	32.4	206	Н	HSTRIR	histone H1 - rainb
23	132	32.3	248	н	HSUR1P	HI,
24	131	32.0	208	~	T23778	H1.1
25	130.5	31.9	220	~	A28456	histone H1.10 - ch
56	130.5	31.9	243	~	AE1689	hypothetical prote
27	129.5	31.7	924	~	T06636	hypothetical prote
28	129.5	31.7	1403	~	T11583	transla
53	129	31.5	218	7	A23055	histone H1.01 - ch

4.

60 KYKA--EAAKKAYKAEAAKAAAKEAA 83

g ò

RESULT 2 AG0592

hypothetical prote histone H1 - musco	histone H1-II - Vo	histone H1 (clone	cgcr-4 protein - C	histone H1 (clone	histone H1.02 - ch	histone H1.03 - ch	conserved hypothet	hypothetical prote	histone H1 homolog	histone H1.11L - c	tolA protein VC183	histone H1B - Afri	histone H1B - Afri	hypothetical prote
T17698 S01262	JN0748	T06241	819113	T06257	HSCH1	D28456	E75383	T06635	861926	B28456	A82152	HSXL1B	I51447	T22455
01 01	~	~	7	N	Н	~	N	N	N	N	0	-	N	0
311	241	284	265	288	218	224	581	606	182	225	356	219	220	581
31.2	30.9	30.9	30.8	30.8	30.7	30.7	30.6	30.4	30.3	30.2	30.1	30.0	30.0	30.0
127.5	126.5	126.5	126	126	125.5	125.5	125	124.5	124	123.5	123	122.5	122.5	122.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

```
C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002
C;Accession: UV0657; B64810
R;Levengood, S.K.; Webster, R.E.
A;Levengood, S.K.; Webster, R.E.
A;Title: Nucleotide sequences of the tolA and tolB genes and localization of their production number: JV0057, MUID:90078104; PMID:2687247
A;Accession: UV0657
A;Accession: UV0657
A;Residues: 1-421 <LEV>
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:MZ8232; NID:g148018; PIDN:AAA24683.1; PID:g148019
A; Experimental source: strain JM105
A; Note: the authors translated the initiation codon GTG for residue 1 as Val
A; Note: the authors translated the initiation codon GTG for residue 1 as Val
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960; A;Experimental source: strain K-12, substrain MG1655
C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
40.1%; Score 164; DB 2; Length 421;
Best Local Similarity 59.3%; Pred. No. 4.8e-05;
Matches 51; Conservative 7; Mismatches 18; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 KEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAA-----KAEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-421 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Map position: 17 min
A;Start codon: GTG
C;Keywords: nucleotide binding; P-loop; transmembrane protein
F:14-34/Domain: transmembrane #status predicted <MSS>
F;78-301/Domain: helical #status predicted <HSR>
F;355-362/Region: nucleotide-binding motif A (P-loop)
tolA protein - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: tolA
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Tola protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83525
R;Stover, C.K.; Pham, Brady, L.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.; Actory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MulD:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: GB:AE005174; NID:g12513672; PIDN:AAG55075.1; GSPDB:GN00145; UWGP:Z09
A,Experimental source: strain 0157:H7, substrain EDL933
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156211; PMID:11258796
                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Nov-2001
C;Accession: G85576
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKEKAYA----KKAEKAY----KKAEAKAYKAAEAKKKAKAEA----KKYAKAA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 37.9%; Score 155; DB 2; Length 394; al Similarity 53.1%; Pred. No. 0.0002; 51; Conservative 6; Mismatches 23; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 155; DB 2; Length 39
Pred. No. 0.0002;
6; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 даёк---даарккадаёкадарккадакадакад 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 KAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.1%;
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-394 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Status: preliminary A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: EC80774
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                          C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AG0592
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J; Churcher, th, T; Connetron, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; PMID:11677608
A;Accession: AG0592
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <PAR>A;Residues: 1-376 <PAR>A;Residues: 1-376 <PAR>A;Genetics:
A;Genetics:
A;Genetics:
   enterica serovar Typhi (strain CT18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane spanning protein TolA [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: F90725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable erythrocyte-binding protein MAEBL - Plasmodium yoelii
C:Species: Plasmodium yoelii
C:Species: Dlasmodium yoelii
C:Accession: T09127
R:Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
Proc. Natl. Acad. Sci. U.S.A. 95, 1938
A;Title: A family of chimeric erythrocyte binding proteins of malaria parasites.
A;Reference number: Z16577; MUID:98115903; PMID:9448314
A;Reference number: Z16577; MUID:98115903; PMID:9448314
A;Status: proliminary; translated from GB/EMBL/DDBJ
A;Status: proliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:AF031886; NID:g2947227; PID:g2947228
A;Experimental source: subspecies yoelii; strain YM
C:Genetics:
A;Gene: maebl
A;Introms: 62/1; 1648/1; 1674/2; 1697/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKEKAYAKKAEKAAKKAEAKAYK-AAEAKKKAKAKAEAKKYA----KAAKAEKKEYA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cch 38.5%; Score 157.5; DB 2; Length 376; al Similarity 54.8%; Pred. No. 0.00013; 51; Conservative 10; Mismatches 17; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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Pred. No. 0.00047;
9; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 AEKKEYAA--AEAKYKAEAAKKA----YKAEAAKAAAKE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 AAEAKKKAEAEAAKAAADAKKKADAEAAKAAAE 217
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Local Similarity 53.5%;
les 53; Conservative
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Best Local Similarity
Matches 51; Conserva
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D.J.; Mayhew K.; Apodaca,

4

Query Match Best Loca Matches

8 유 ð RESULT 4

substrain

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Query Match 36.1%;
Best Local Similarity 45.2%;
Matches 47; Conservative
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A Molecule type: DNA
A Residues: 1-388 < KUR>
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Matches
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histone H1 - sea urchin (Lytechinus pictus)
histone H1 - sea urchin (Lytechinus pictus)
histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
C;Accession: A25550
C;Accession: A25550
Nucleic Acids Res. 14, 8121-8133, 1986
A.Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus an A;Reference number: A25550; MUID:87040778; PMID:302245
A;Accession: A25550
A;Accession: A25550
A;Accession: A25550
A;Residues: 1-210 - KNOD-
A;Residues: 1-210 - KNOD-
A;Residues: 1-210 - KNOD-
C;Superfamily: histone H1
C;Seywords: chromosomal protein; DNA binding; nucleosome; nucleus
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A; Cross-references: EMBL:U16726
A; Cross-references: EMBL:U16726
A; Note: the authors did not translate the codon for residue 1
R; Fabry, S.; Ford, C.; Lindauer, A.; Mueller, K.; Cornelius, T.; Schmitt, R. submitted to the EMBL Data Library, October 1994
A; Description: The organization, structure and controlling elements of Chlamydomonas his
                                                                                                               A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: tolA; PA0971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAA------EAKKKAKAEAKKYA---- 44
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                                                                                                                                                                                                                                                                                                                     Length 347;
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36.9%; Score 151; DB 2; Length 210
Best Local Similarity 51.7%; Pred. No. 0.00024;
Matches 46; Conservative 10; Mismatches 25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 --KAAKAEKKEYAAAEAKYKA--EAAKKAYKAEAAKAAAKEAA 83
                                                                                                                                                                                                                                                                                                                Query Match
37.7%; Score 154; DB 2;
Best Local Similarity 47.6%; Pred. No. 0.00021;
Matches .49; Conservative 11; Mismatches 21;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <STO>
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R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I. Nature 413, 523-527, 2001

A.Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A.Reference number: AB0001; MUID:21470413; PMID:11586360
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamili, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Auchors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome : A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Cross-references: GB:283018; GB:AL123456; NID:g3261671; PIDN:CAB05427.1; PID:g1694845
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TolA colicin import membrane protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AL590842; PIDN:CAC89966.1; PID:g15979190; GSPDB:GN00175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable hupB - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 20-Jun-2000
A;Residues: 1-173,'P',174-231 <FAW>
A;Cross-references: EMBL:U16726; NID:g571479; PIDN:AAA98452.1; PID:g571480
C;Genetics:
A;Introns: 62/3; 101/3
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 AKKAATPKKAAAPKKEGAVKKTKAPKKEGEKKPKSAKKAEKKPKKEGEKKKAAKPAKAEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAYAKKAEKAAKKAEA------KAYKAAEAKKKAKAEAKKYAKAAEK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEAKYKAEAAKKAYKAEAAKAAAKEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
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                                                                                                                                                                                                                                                                             Length 231;
                                                                                                                                                                                                                                                                                                                                             29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 EVAEKAAADAAEKKAAADAEKKAAAAKKVAAAAEAKKAAAEAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 147.5; DB 2;
Pred. No. 0.00067;
9; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 ------YAAAEAKYKAEAAKK-AYKAEAAKEAA
                                                                                                                                                                                                                                                                     7 Match 36.4%; Score 149; DB 2; Local Similarity 39.5%; Pred. No. 0.00035; Les 47; Conservative 7; Mismatches 29;
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKA-EKKEYAAAEA 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: tolA
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
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Matches
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                                                                                                                                                                                                                                                                                                                                                         RESULT 11
A28100
A28100
C; Secies: Strongylocentrotus purpuratus)
C; Species: Strongylocentrotus purpuratus)
C; Species: Strongylocentrotus purpuratus
C; Species: Strongylocentrotus purpuratus
C; Accession: A8100
B; Lai, Z.C.; Cthids, G.
Mol. Cell. Biol. 8, 1842-1844, 1988
A; Pitle: Characterization of the structure and transcriptional patterns of the gene encontrol of the structure and transcriptional patterns of the gene encontrol of the structure and transcriptional patterns of the gene encontrol of A; Reference number: A28100; MUID:88246461; PMID:2837660
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-211 cLAI>
A; Residues: 1-211 cLAI>
A; Cross-references: GB:M20314
C; Superfamily: histone H1
C; Keywords: chromosomal protein; DNA binding; embryo; nucleus
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mst101-1 protein - fruit fly (Drosophila hydei)

C;Species: Drosophila hydei
C;Species: Drosophila hydei
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34153
R;Nedsen, J; Heinlein, U.A.O.; Buenemann, H.
Bubmitted to the EMBL Data Library, June 1993
A;Reference number: S34153
A;Reference number: S34153
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                     111 AKKVAK--KAPAKKATKAAKKAATKAPARKAATKAPAKKAATKAPAKKAVKATKSPAKKV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 KSDAQKARDAAKKAKTAAKKEAKEKKAARSKAKKEKLAAKKASK--KTTKKVKKPAAKK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 AKK--EKEAAEKKCAEAAKKEKEAAEKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEK 122
                                                                                                                  Gaps
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                                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKAKAEAKKYAKAAKAEKKEY
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                                                                     Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 144; DB 2; Length 211;
Pred. No. 0.00074;
6; Mismatches 29; Indels
                                                                                                                34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-344 <NEE>
A;Cross-references: EMBL:X73480; NID:g313199; PID:g313200
C;Genetics:
                                                                  Score 147; DB 2;
Pred. No. 0.00046;
3; Mismatches 34;
                                                                                                                                                                                                                                                                               169 TKAVKKTAVKASVRKAATKAPAKKAAAKRPATKA 202
                                                                                                                                                                                                                                                     55 AAAEAK--YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: FlyBase:FBgn0011816
C;Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 AKKPAAKKAAKKPAAKKPAAKKAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YKAEAAKKAYKAEAA-KAAAKEAA 83
                                                                  35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.2%;
                                                                                                                Conservative
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Matches 45; Conservative
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A;Gene: hupB
C;Superfamily: histone H1
                                                                Query Match
Best Local Similarity
Matches 47; Conserve
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es 49; Conserv
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Best Local S
Matches 49
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A,Cross-references: GB:U32722, GB:L42023, NID:g1573348, PIDN:AAC22041.1; PID:g1573353; TJI R,Sen, K.; Sikkema, D.J.; Murphy, T.F. Gene 178, 75-81, 1996
A,Ttle: Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA and A,Reference number: JC5212; MUID:97080550; PMID:8921895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: UC5212
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 'V';2-47,'A',49-141,'R',143-164,'P',166-189,'R',191-202,'A',204-226,'A',228-5
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Cispecies: Ramdon, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocayne, J.D.; Scott, J. Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Accession: G64064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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A; Note: the authors translated the codon CGT for residue 190 as Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Status: nucleic acid sequence not shown; translation not shown A,Molecule type: DNA A,Residues: 1-372 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Indels
                                                     123 KKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKE 164
8
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50.0%; Pred. No. 0.0018;
cive 11; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.7%; Score 142; DB 2; 52.1%; Pred. No. 0.0016; iive 9; Mismatches 22
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C; Superfamily: neurofilament triplet H protein
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Spinson tail-specific protein mst101(2) - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
S; Blochem. 25, 1089-1095, 1994
A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represe
A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represe
A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represe
A;Title: Tandemly arranged repeats of the novel
A;Recence number: S31364; MUID:95045538; PMID:7957199
A;Accession: S51364
A;Accession: S51364
A;Cross-reference number: S34153
A;Residues: 1-1390 «NEB.
A;Residues: 1-130, R. J. Heinlein, U.A.O.; Buenemann, H.
Submitted to the EMBL Data Library, June 1993
A;Residues: 1-163, E', 164-236, 'Q', 237-254,257-320,'E', 321-1390 «NEW.
A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
C;Genetics:
A;Genetics:
A;Gene: mst101(2)
A;Cross-references: FlyBase: FBgn0011816
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24; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

34.4%; Score 140.5; DB 2; Length 1390;
Best Local Similarity 46.2%; Pred. No. 0.0055;
Matches 48; Conservative 9; Mismatches 23; Indels 24;
                                                                                                                                                         167 TKVAEAEKQKAAEATKVAEAEKQKAAEA 194
                                                                                                            60 KYKAEAAK-KAYKAEAAKAAAKEAAYEA 86
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Search completed: March 10, 2003, 12:28:29 Job time : 26.2194 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

March 10, 2003, 12:15:01 ; Search time 19.5949 Seconds
 (without alignments)
182.035 Million cell updates/sec Run on:

US-09-816-989A-6 409 1 AKKYAKKEKAYAKKAEKAAK.......KRYKAEAAKAAAKEAAYEA 86 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	ion	escherichia	pseudomonas	lytechinus	mycobacteri	mycobacteri	drosophila	haemophilus	strongyloce	drosophila	strongyloce	aedes aegyp	aedes albop	mycobacteri	treponema	saccharomyc	oncorhynchu	parechinus	caenorhabdi	gallus gall	schizosacch	gallus gall	klebsiella	anas platyr	volvox cart	gallus gall	gallus gall	gallus gall	xenopus la	chironomus	triticum a	homo sapien	gallus gall	chironomus
	Description	P19934 e		P06144 1	P95109 m				P15869 B	Q08696 d		Q9u761 a		Q9zhc5 m			P06350 O			-					Q08865 V	P09987 g				P40278 c		P16401 h	P12957 g	P40276 cl
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SUMMARIES	•	TOLA ECOLI	TOLA PSEAE	H1 LYTPI	DBH MYCTU	DBH MYCBO	MST1 DROHY	TOLA HAEIN	B STRPU	TZ DROHY	HIG STRPU	6 AEDAE	6 AEDAL	DBH MYCSM	IPB TREPH	ZUO1_YEAST	ONCMY	PARAN	1 CAEEL	.10_CHICK	YDF3_SCHPO	.01_CHICK	R KLEPN	ANAPL	2 VOLCA	H1 CHICK	03 CHICK		H1B_XENLA	HIE CHITE	WHEAT	H15 HUMAN	CALD CHICK	H1B_CHITE
	DB ID	1	1 4	1 H1	1	1 0	1 MS	1 7	1 H	1 M.	1 H	1 R5	1 R5	1 DE	i i	1 ZI	1 H	1 H	1 H	1 H	1 XI	1 H	1 AS	1 H	1 H	1 H	1 H	H	1 H	1 H	1 H	1 3	5	T =
	Length D	421	347	210	214	205	344	372	211	1391	217	346	349	208	384	433	206	248	207	219	1403	21.8	139	217	240	217	223	224	219	237	238	225	771	232
de	Query Match	40.1	37.7	36.9	35.9	35.8	34.8	34.7	34.5	34.4	33.7		33.5	33.4	32.6	32.6	32.4	32.3	32.0	31.9	31.7	31.5		30.9	30.9			30.2	ö	φ.	φ.	ď	29.2	29.3
	Score	164	154	151	147	146.5	142.5	142	141	140.5	138	137.5	m				132.5	132	-	130.5	129.5	129	127	126.5	126.5	125.5	125.5	123.5	122.5	121.5	121.5	121	120.5	120
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P19649 treponema p P02254 salmo trutt P08288 gallus gall P40277 chironomus Q07134 chironomus P10412 homo sapien P4026 glyptotendi P57873 pasteurella P6892 xenopus lae P15866 xenopus lae P15867 drosophila
TWPB TREPA H1 SALTR H1E CHICK H1C CHITE H1C CHITH H14 HUMAN H11 GLYSA IP2 PASMU H1A XENLA H1C IXBNLA H11 GLYBA H11 GLYBA
<b>аааааааааа</b>
325 194 194 2218 233 209 233 233 233
777772 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
120 118.5 118 118 118 117 116.5 115.5 115.5
UUUUUU44444444444444444444444444444444

# ALIGNMENTS

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MEDLINE=97113525; PubMed=8955385;
                                                                                                                                 REVISIONS TO N-TERMINUS
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37
347
216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lytechinus.
NCBI_TaxID=7653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Sin
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    RRARA 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 KAEADAKAAEBAAKKAAADAKKKAEAEAAKAAAEAQKKAEAAAAALKKKAEAAEAAAEA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 KEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAA-----KAEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                              OF BACTERIOPHAGE DNA.
SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, OMPC, PHOE
                                                                                                                                                                                                                                                                                                                                      AND LAMB. -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fransport; Protein transport; Bacteriocin transport; Transmembrane;
                                                                                              MEDLINE-99312679; Pubmed-10404600;
Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.;
Filamentous phage infection: crystal structure of g3p in complex with its coreceptor, the C-terminal domain of Tola.";
Structure 7:711-722(1999).
-- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A COLICINS (COLICINS A, E1, E2, E3, AND K). NECESSARY FOR THE COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERIPLASMIC (POTENTIAL).
DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                     "TolA central domain interacts with Escherichia coli porins."; EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.1%; Score 164; DB 1; Length 421; 59.3%; Pred. No. 2.5e-05; tive 7; Mismatches 18; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; Inner membrane; 3D-structure; Complete proteome. DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (2,4).
8B2F52B4B97C655E CRC64;
                                                                                   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 RKKAATEAAEKA-KAEAEKKAAAEKA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 KYKA--EAAKKAYKAEAAKAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AECOGOT77, AEC73833.1; -.
EMBL, D90713, BAA35405.1; -.
PIR, JV0057, JV0057.
PDB; 1TOL; 20-MAY-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 AA; 43156 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M28232; AAA24683.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB; 1TOL; 20-MAY-99.
EcoGene; EG11007; tolA.
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34
421
310
421
278
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TOLA OR PA0971.
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Lloubes R.;
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Best Local S
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TOLA PSEAE
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  셤
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE004530; AAG04360.1; -.
Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                     of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Indels
Dennis J.J., Lafontaine E.R., Sokol P.A.,
                                                                                                                                                                                                         Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 347 PERTPLASMIC (POTENTIAL).
209 216 POLY-ALA.
347 AA; 37935 MW; EEDD4B04AA095945 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
PERIPLASMIC (POTENTIAL).
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Pred. No. 0.00011;
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AC POG_144,
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-JAN-1999 (Rel. 38, Last amoneation update)
DF 15-JUL-1999 (Rel. 38, Last amoneation update)
DF 15-JUL-1999 (Rel. 38, Last amoneation update)
DF 16-JUL-1999 (Rel. 38, Last amoneation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAOl;
MEDLINE=20437337; PubMed=10984043;
                                                                    Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.7%;
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EMBL; AE004530; AAG04360.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opportunistic pathogen.";
Nature 406:959-964(2000).
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=H37Rv;
                                                                                                                                                                                                        Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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   SO THE REAL PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglaneier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HISSP, P02259, 1HST.
InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist N.
Pfam, PF00538; linker-histone; I.
SMART; SM00526; H15; I.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 210 AA; 21746 MW; 08C38F64894007E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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15-JUL-1999 (Rel. 38, Last sequence update)
16-CT-2001 (Rel. 40, Last sequence update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp) (21-kDa laminin-2-binding protein)
HWP OR HLP OR LEB21 OR WY2986G OR MT3064 OR MTCY349.01.
Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBI_TaxID=1773;
                                                                                                                                 Lytechinus pictus and Strongelocentrotus purpuratus.";
Nucleic Acids Res. 14:8121-8133(1986).
-!- FUNCTION: HISTONES H1 ARB NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8;
                         MEDLINE-87040778, PubMed-3022245,
Knowles J.A., Childs G.J.;
"Comparison of the late H1 histone genes of the sea urchins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.9%; Score 151; DB 1;
51.7%; Pred. No. 0.00012;
ative 10; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 КРАККААККРААККААККРААККРАККАА 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YKAE-----AAKKAYKAEAAKAAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X04488; CAA28177.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=H37Rv
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn N.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Savita P.;
Submitted (DEC-1997) to the SWISS-PROT data bank.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILLEE IT, AND PREVENT ITS DENATURATION UNDER EXTREME
BNVIRONMENTAL CONDITIONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 AKKVAK--KAPAKKATKAAKKAATKAPARKAATKAPAKKAATKAPAKKAVKATKSPAKKV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DBH WYCBO STANDARD; PRT; 205 AA.

(9XEL18; 09S515;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp).
Mycobacterium bovis.

Mycobacteria, Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteridae;
NCBI_TAXID=1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKAKAEAKKYAKAAKAEKKEY 54
                                                                                                                                                                                                                                                    "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pragad H.K., Annapurna P.S., Dey A.B., Tyagi J.S., Jain N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PP00216; Bac_DNA binding; 1.
PRINTS; PR00624; HISTONEHS.
ProDom; PD000945; Bac_DNAbind; 1.
PROSITE; PS00041; BHL; 1.
PROSITE; PS00045; HISTONE_LIKE; 1.
DNA-binding; DNA condensation; Repeat; Complete proteome.
DOMAIN 10 214 BACTERIAL HISTONE-LIKE DOMAIN.
SEQUENCE 214 AA; 22187 MW; CB09AP20FB353544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.9%; Score 147; DB 1; Length 214; 50.0%; Pred. No. 0.00023; Live 3; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                              laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 TKAVKKTAVKASVRKAATKAPAKKAAAKRPATKA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuberculist; Rv2986c; -. InterPro; IPR000119; Bac DNAbind. InterPro; IPR001386; Histone H1/H5.
                                                                                                                                                                                                                                                                                                                                                                          [3]
SEQUENCE OF 71-86, AND DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z83018; CABO5427.1; -.
EMBL; AE007127; AAK47393.1; -.
HSSP; P02346; 1HUU.
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MEDLINE=94200512; PubMed=8150205;
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TOLA OR HI0383
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                  from Mycobacterium.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                    Prabhakar S., Tyagi J.S., Prasad H.K.; "HLPMt-A target for differentiation of M.tuberculosis and M.bovis."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 AKKVAK--KAPAKKATKAAKKAATK----APAKKAATKAPAKKAVKATKSPAKKVTKAVK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MST101(1).
Drosophila hydei (Fruit fly).
Eukaryophila Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Eukaryota; Metazoa; Archtera; Endopterygota; Diptera; Brachycera;
Insecta; Pterygota; Neoptera; Endopterygota; Drosophila.
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKA-KAEAKKYAKAAKAEKKEYAAAEA 59
                                                                                                        STRAIN=BCG / Tokyo;
Matsumoto S., Yukitake H., Matsuo T., Mineda T., Yamada T.;
"Identification of a novel protein generating bacterial slow growth
                                                                                                                                                                                                                                                                                                                                                                                            REMBL; ABULSTT.

R HSSP; PO2346; IHUU.
R InterPro; IPR001136; Histone H1/H5.
R Fefan; PF00216; Bac DNA binding; 1.
DR PF00016; Bac DNA binding; 1.
DR PROMO$45; Bac DNA binding; 1.
DR PROMO$45; HISTONE LIKE; 1.
DR PROSTIE; PS00045; HISTONE LIKE DOMAIN.
DNA-binding; DNA condensation; Repeat.
BACTERIAL HISTONE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.8%; Score 146.5; DB 1; Length ilarity 53.9%; Pred. No. 0.00024; Conservative 3; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEGENERATE REPEATS REGION.
A -> T (IN REF. 2).
19FCE67885DFE6A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Axoneme-associated protein mstl01(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 KTAVKASVRKAATKAPAKKAAAKRPATKA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 K--YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB013441; BAA78330.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 199 A
205 AA; 21262 MW;
                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y18421; CAB46493.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
             FROM N.A.
                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                           STRAIN=ANS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MST1 DROHY Q08695;
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Neesen J., Buenemann H., Heinlein U.A.;
"The Drosophila hydei gene.Dhmstill(!) encodes a testis-specific,
repetitive, axoneme-associated protein with differential abundance in
Y chromosomal deletion mutant flies.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN=RG / KW20 / ATCC 51907;

MEDLINE=95350630; Dubmed=752800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,

McKennavg R., Sutton G., Fitzhugh W., Fields C.A., Goozyne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Gnehm C.L., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKAYAKKAEKAAKKAE--AKAYKAAEAKKKAK--AEAKKYAKAKAE----- 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sperm, Repeat; Multigene family.

19 X 16 AA APPROXIMATE TANDEM REPEATS
19 X 16 AA APPROXIMATE TANDEM REPEATS
19 X 16 AA AE-X-C-X-E-X-A-[KQ]-K-X-X-E-X-A-X.

SEQUENCE 344 AA, 37793 MW; 24C65D2510387E2A CRC64;
                                                                                                                                                      Dev. Biol. 162:414-425(1994).
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL. IT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                        SPERMATID BUNDLES.
-!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
-!- POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN STRAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 344;
                                                                                                                                                                                                                             ASSOCIATED WITH AXONEMAL STRUCTURES.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUE SPECIFICITY: TESTIS. LOCATED IN SPERMATOCYTES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.8%; Score 142.5; DB 1; Length 48.0%; Pred. No. 0.00069; tive 7; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 ККСАЕДАККЕКЕДАЕКККСАЕДАККЕКЕДАЕКККСАЕДАККЕ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 -----KKEYAAAEAKYKAEAAKK----AYKAEAAKAAAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P44678; P94810;
01-NOV-1995 (Rel. 32, Created)
10-NOV-1995 (Rel. 32, Last sequence update)
10-LON-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, X73480; CAA51875.1; -.
PIR, S34153; S34153.
FlyBase; FBgn0011816; Dhyd\mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Query Match
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                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Buechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYA-----KKEKAYAKKAEKAAKK----AEAKAYKAAEAKKKAKAEAKKYAKAEK 51
                                                                                                                                                                                                                                                                         Transport; Protein transport; Transmembrane; Repeat; Inner membrane;
                               Sen K., Sikkema D.J., Murphy T.F.;
"Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA and tolB genes.";
Gene 178:75-81 (1996).
                                                                          -i - FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS (BY SIMILARITY).
-i - SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                        AKANABAKAKA (IN STRAIN 1479).
A (IN STRAIN 1479).
F (IN STRAIN 1470).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 372;
                                                                                                                                                                                                                                                                                                                                                    (IN STRAIN 1479).
(IN STRAIN 1479).
(IN STRAIN 1479).
(IN STRAIN 1479).
                                                                                                                                                                                                                                                                                                                                                                                                                                           -> S (IN STRAIN 1479).
-> A (IN STRAIN 1479).
-> P (IN STRAIN 1479).
266ECF05C6C95544 CRC64;
                                                                                                                                                                                                                                                                                                                                (IN STRAIN 1479)
(IN STRAIN 1479)
                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                   (IN STRAIN 1479)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 142; DB 1;
Pred. No. 0.0008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 14, Created)
(Rel. 14, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 KAKAAAEAKAKADAEAKA--ATEAKRKADQASLD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
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                                                                                                                                                                                                                                                                                                                                   4 K
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                      MEDLINE=97080550; PubMed=8921895;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Histone H1-beta, late embryonic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39831 MW;
                                                                                                                                                                                                                           EMBL; U32722; AAC22041.1; -.
EMBL; U32470; AAC44596.1; -.
HSSP; P19934; ITOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.7%;
52.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                            234
254
254
306
333
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372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strongylocentrotus.
                                                                                                                                                                                                                                                                                     Complete proteome.
FROM N.A.
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                                                                                                                (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7668;
                                                                                                                                                                                                                                                              TIGR; HI0383; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990
01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
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SEQUENCE
                                                                                                                                                                                                                                                                                                          RANSMEM
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VARIANT
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POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
Lai Z.-C., Childs G., "Characterization of the structure and transcriptional patterns of the gene encoding the late histone subtype HI-beta of the sea urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 KSDAQKAPDAAKKAKLAAKKKBAKEKKAARSKAKKEKLAAKKASK--KTTKKVKKPAAKK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK-KKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MST101(2).

Drosophila hydei (Fruit fly).

Bukaryota; Matazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Bukaryota; Metazoa; Arthropota; Budopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 211 AA; 22169 MW; 9F214581334BBE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=95045538; PubMed=7957199;
Neesen J., Padmanabhan S., Buenemann H.;
Tandemly arranged repeats of a novel highly charged 16-amino-acid motif representing the major component of the sperm-tail-specific axoneme-associated protein family Dhmst101 form extended alpha-helical rods within the extremely elongated spermatozoa of
                                                                               Strongylocentrotus purpuratus.";
Mol. Cell. Biol. 8:1842-1844(1988).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAIRS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL.
-I- SUBCELLULAR LOCATION: Cytoplasmic.
-I- TISSUE SPECIFICITY: TESTIS. PRIMARY SPERMATOCYTES AND EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.5%; Score 141; DB 1; Length 211; 53.6%; Pred. No. 0.0006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Axoneme-associated protein mst101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M20314; AAA30052.1; -.
PIR; A28100; A28100.
HSSP; P02259; 1HST.
INTERPRO; IRR001386; Histone H1/H5.
INTERPRO; IRR001316; Linkerhist_N.
PFGM; PF00038; linker histone; 1.
PRODOM; P000037; Linkerhist_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 225:1089-1095(1994)
-i- FUNCTION: POSSIBLE STRUCTURAL RO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 АККРААККААККРААККРААККАА 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKAEAAKKAYKAEAA-KAAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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RS6 AEDAE
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                                                                                                                                                                       185
                                                                 Matches
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Matches
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                                                                                                                                                                                                                                                                                                        1196 AKK--EQEPAEMKKCEEAAKKEKERAAEKÇKCAKAAKKEKERAEK-KKCAEAAKKEGEAAE 1252
                                                                                                                                                                    Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Eucchinoidea, Echinacea, Echinoida, Strongylocentrotidae,
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKKAEKAAKKAE--AKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=87172742; PubMed=3031476;
Knowles J.A., Lai Z.-C., Childs G.J.;
"Isolation, characterization, and expression of the gene encoding t late histone subtype H1-gamma of the sea urchin Strongylocentrotus
                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q.
                                                                                                                                                                                                                                    34.4%; Score 140.5; DB 1; Length 1391; 46.2%; Pred. No. 0.0029; Live 9; Mismatches 23; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1253 KKKCABAAKKEKBAEKKRKCEKABKAALKRQCAKLVIRAKBAA 1296
                                                                                                                                                                                                                                                                                                                                            59 AKYKAEAAKKAYKAE-----AAKAA------AKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE HISTONE HI/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1-gamma, late.
                                                                                                                                          PIR; S34154; S34154.
FlyBase; FBgn0020733; Dhyd\mst101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, P02259; IHST.
InterPro; IPR001366; Histone H1/H5.
InterPro; IPR00216; Linkerhist N.
Mfam; PF00538; linker histone; I.
ProDom; PD000373; Linkerhist N; 1.
SMARTI, SM00526; H15; 1.
                                                                                                                               EMBL; X73481; CAA51876.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M16033; AAA30059.1; -.
                                                                                                                                                                                                                                                               48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strongylocentrotus.
NCBI_TaxID=7668;
REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                   H1G STRPU
P07796;
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gavino V.H., Fallon A.M.;

"Aedes mosquitoes ribosomal protein S6 cDNA.";

"Aedes mosquitoes ribosomal protein S6 cDNA.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: MAY PLAY AN IMPORTANT'ROLE IN CONTROLLING CELL GROWTH

-!- AND PROLIFERATION THROUGH THE SELECTIVE TRANSLATION OF PARTICULAR

CLASSES OF MRNA (By similarity).

-!- FTM: Ribosomal protein S6 is the major substrate of protein

kinases in eukaryote ribosomes (By similarity).

-!- SIMILARITY: BELONGS TO THE S6E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
                                                                                                                                                                                                          2 KKYAKKEKAYAKKAEK------AAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family. SEQUENCE 217 AA; 22658 MW; C7251EED3413B185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKE-KAYAKKAEKAAKKAEAKAYKAAEAKK-KAKAEAKKYAKAAKAEKK-EYAAA
                                                                                                                                                  14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 346;
                                                                                     217;
                                                                                                                                               30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribosomal protein; Phosphorylation.
SEQUENCE 346 AA; 39365 MW; 599CFF7B22BD8DFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Match 33.6%; Score 137.5; DB 1; Local Similarity 51.1%; Pred. No. 0.0016; ne 45; Conservative 5; Mismatches 33;
                                                                Score 138; DB L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
40S ribosomal protein 86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 AA
                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                            50 EKKEYAAAEAKYKAEAAKKAYKAEAAKAAKEA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 PAVAKKEAPKR--KPEAAKGDASAAKKE 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aedes aegypti (Yellowfever mosquito)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF154067; AAF04790.1; -.
InterPro; IPR001377; Ribosomal_S6E.
Pfam; PF01092; Ribosomal_S6e; I.
ProDom; PD003460; Ribosomal_S6E; I.
PROSITE; PS00578; RIBOSOMAL_S6E; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 EAKYKAEAAKKAYKAEAAKAAAKEAAYE
                                                                                     33.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                  43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                        Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TREPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
TMPB_TREPH
  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Gavino V.H., Fallon A.M.;

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN CONTROLLING CELL GROWTH
AND PROLIFERATION THROUGH THE SELECTIVE TRANSLATION OF PARTICULAR

CLASSES OF MRNA (By similarity).

-!- PTM: Ribosomal protein $6 is the major substrate of protein

kinases in eukaryote ribosomes (By similarity).

-!- SIMILARITY: BELONGS TO THE $6E PAMILY OF RIBOSOMAL PROTEINS.
                                                                                                               Aedes albopictus (Forest day mosguito).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Aedes.
NCBI_TAXID=7160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 AKKVAKKEAKKEVKKVTEAAKKADAKAAKAKVEPKKADKKSADSGKKATAGDKKEKKVEK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKE-KAYAKKAEKAAKKAEAKAYKA----AEAKKKAKAEAKKYAKAAKAEKK-EY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 700084 / mc(2)155;
MEDLINE=99110209; PubMed=9894918;
Lee B.H., Mirugasu-Oei B., Dick T.;
"Upregulation of a histone-like protein in dormant Mycobacterium smegmatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 137; DB 1; Length 349;
Pred. No. 0.0017;
5; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
Le-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosomal protein; Phosphorylation.
SEQUENCE 349 AA; 39619 MW; 669A5DA33F8BADD3 CRC64;
                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
40S_ribosomal protein S6.
     349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 KAAPAAKKEAPKR--KPEAAKGDASAAKKE 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 AAAEAKYKAEAAKKAYKAEAAKAAAKEAAYE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF154066; AAF04789.1; -.
InterPro; IPR001377; Ribosomal S6E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01092; Ribosomal S6e; I.
ProDom; PD003460; Ribosomal S6E; I.
PROSITE; PS00578; RIBOSOWAL_S6E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 49.5
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DBH MYCSM
Q9ZHCS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR HLP
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AC DBH N
DT 16-0C
DT 16-0C
DT 16-0C
DE DNA-1
GN MYCOD
OC BACT!
OC BACT!
OC BACT!
OC ACTIN
TRP [1]
RN [1]
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RC STRA
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RX MEDI
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Mol. Gen. Genet. 260:475-479(1998).

-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOUTC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell F., Sliviensky L., Schouls L.M., van Embden J.D., Charon N.W.; "Treponema phagedenis encodes and expresses homologs of the Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKK---EKAYAKK--AEKAAKKAEAK--AYKAAEAKKKAKAEAKKYAKAEKA-- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pallidum TmpA and TmpB proteins.";
Infect. Immun. 59:3685-3693(1991).
-!- FUNCTION: TMP MAY SERVE AS A PORIN OR TRANSPORT PROTEIN FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Repeat.
DOMAIN 1 90 BACTERIAL HISTONE-LIKE DOMAIN.
NAMAIN 101 205 DEGENERATE REPEATS RECTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.4%; Score 136.5; DB 1; Length 51.6%; Pred. No. 0.0012; tive 6; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CASF577F61F7EF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Treponemal membrane protein B precursor (Antigen tmpB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Spirochaetales, Spirochaetaceae, Treponema.
NCBI_TaxID=162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: OUTER MEMBRANE-ASSOCIATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 KEYAAAEAKYKAEAAKKAYKAEAAKAAAKEA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P02346; IHUU.
InterPro; IPR000119; Bac DNAbind.
Pfain; PF00216; Bac DNA bInding; 1.
ProDom; PD000945; Bac DNA binding; 1.
SWART; SM00411; BHL; IBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91372983; PubMed=1894368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF068138; AAD13809.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 AA; 21230 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 51.6
Matches 47; Conservative
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                                                                                                                             1-10.
1-11.
1-12.
1-13.
1-15.
1-16.
1-17.
6 X 8 AA TANDEM REPEATS OF [EA]-A-A-R-X-A-A-B.
                                     TREPONEMAL MEMBRANE PROTEIN B.
17 X 5 AA TANDEM REPEATS OF K-A-A-[AKR]-
                                                                                                                                                                                                                                                                                                               5; Gaps
                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKKA--EKAAKK--AEAKAYKAAEAKKKAKAEAKKYAKAAKAE-KKEYA 55
                                                                                                                                                                                                                                                                                                                                                                                                                               ZUOI OR YGR28SC.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                   Score 133.5; DB 1; Length 384;
Pred. No. 0.0032;
9; Mismatches 30; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang S., Lockshin C., Herbert A., Winter B., Rich A.;
"Zuotin, a putative Z-DNA binding protein in Saccharomyces
                                                                                                                                                                                                                                                      6E94CBC74294DE8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                    9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 1-10
                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                        56 AAEAKYKAEAAKKAYKAEAAKAAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=20B-12;
MEDLINE=93010971; PubMed=1396572;
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STRAIN=S288c / FY1679;
MEDLINE=97245295; PubMed=9090054;
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                       Antigen; Outer membrane; Repeat;
                                                                                                                                                                                                                                                     42677 MW;
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       EMBL; M58563; AAA27480.1;
PIR; B43592; B43592.
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Best Local 44; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Volckaert G., Voet M., Robben J.;
"Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the right arm of chromosome VII from Saccharomyces cerevisiae carrying the MAL1 locus reveals 15 complete open reading frames, including ZUO1, BGL2 and BIO2 genes and an ABC transporter gene.";
Yeast 13:251-259(1997).
-i- FUNCTION: Z-DNA BINNIOF PROTEIN. COULD BE INVOLVED IN CHROMOSOME ORGANIZATION.
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, 0AA76BC11D3C7DAB CRC64;
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PIR; S25194; S2517; S2017; S2017
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-!- SIMILARITY: CONTAINS 1 J DOMAIN.
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-816-989A-6 409 Title: Perfect score: Sequence:

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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 Total number of hits satisfying chosen parameters:

671580 segs, 206047115 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

Sp\_plant:\*
Sp\_rodent:\*
Sp\_virus:\*
Sp\_virus:\*
Sp\_vertebrate:\*
Sp\_unclassified:\*
Sp\_rirus:\*
Sp\_bacteriap:\*
Sp\_archeap:\* SPTREMBL 21:\*

1: 8p\_archea:\*
2: 8p\_bacteria:\*
3: 8p\_fungi:\*
4: 8p\_human:\*
5: 8p\_human:\*
6: 8p\_mammal:\*
7: 8p\_mhc:\* sp\_organelle:\* sp\_phage:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Q8zqt6 salmonella	O9wwx1 pseudomonas	Q8z8c1 salmonella	O61164 plasmodium	Q8x965 escherichia	Q937k4 erwinia chr	Q98kg7 rhizobium 1	Q39576 chlamydomon	Q9cm70 pasteurella	Q8zgz2 yersinia pe	Q8t5c8 plasmodium	Q8xvn7 ralstonia s	Q26947 trypanosoma	093946 candida alb	090zd7 bufo bufo q	Q93901 caenorhabdi
ΩI	Q8ZQT6	Q9WWX1	08Z8C1	061164	96X80 9	Q937K4	. Q98KG7	039576	6 Q9CM70	. Q8ZGZ2	Q8T5C8	S QBXVN7	Q26947	093946	1 Q90ZD7	093901
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% Query Match	40.5	39.9	38.5	38.3	37.9	37.7	36.9	36.3	36.2	36.1	35.7	34.0	33.6	32.9	32.2	32.0
Score	165.5	163	157.5	156.5	155	154	151	148.5	148	147.5	146	139	137.5	134.5	131.5	131
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Q92A67 O01395 Q8RXD0 Q9SU08 Q9FP71	Q8T5C9 Q8WQ44 Q8T9R3 Q9XHL9	Q84528 Q95S18 Q65794 Q39598 Q65795		Q52088 Q9V6S7 O46142 Q9KR10 O46141	046362 Q9SWU2 Q9ZR20 Q9AT22 Q9SXQ8
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# ALIGNMENTS

T 1  6  6282076  6  6282076  101-MAR-2002 (TrEMBLrel. 20, Created)  101-MAR-2002 (TrEMBLrel. 20, Last sequen)  101-MAR-2002 (TrEMBLrel. 21, Last annotes and representations of STM0741.  101 protesin, membrane spanning protein. Salmonella typhimurium.  Bacteria; Proteobacteria; gamma subdivi Salmonella.  101 TaxID=602;  102 MBDLINE=21534948; PubMed=11677609;  MEDLINE=21534948; Pallones and Salmonella and Salmo	PRT; 407 AA. eated) st sequence undate)	21, Last annotation update) panning protein.	Joua On Simoly Brythimurium. Salmonella typhimurium. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.		00720; 609; Sosieth J., Clifton S.W., Latreille P.,	Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Mayven C., Scott K., Holmes A., Grewal N., Mulvaney B., Rvan R. Sun H. Florea L. Miller W. Stoneking T. Nhan M.	Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium			2534352116602D75 CRC64;	Score 165.5; DB 16; Length 407; Pred. No. 2.5e-05; 14; Mismatches 16; Indels 21; Gaps	1 AKKYAKKEKAYAKKAEKAAKRAEAKAYK-AAEAKKKAKAEAKKYAKAAKAEK 51
T 1  6  6  6  6  6  10MAR-2002  10MAR-11  10MAR-2002  10MAR-2002  10MAR-2003	PRELIMINARY (TrEMBLrel)	MBLrel. brane s	Salmonella typhimurium. Bacteria, Proteobacteria,	NCBI_TaxID=602; [1] SEQUENCE FROM N.A.	/ SGSC1412 / A1 34948; PubMed=1 M Sanderson R	, Porwollik S., Nguyen C., Sco	., Wilson R.K.; enome sequence	LT2."; Nature 413:852-856(2001). EMBL; AE008730; AAL19691.1	FROODING; AUCTI 0308; ANTIFREEZ oteome.		Query Match Best Local Similarity 51.9% Matches 55, Conservative	kkekayakkaekaa  :::  ::       qqqqqaeeaakaal
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"The Pseudomonas purida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity of the cell envelope.";
J. Bacteriol. 178:1699-1706(1996).
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MEDLINE=96422022; PubMed=8824639;

Rodriguez-Herva J.J., Ramos J.;

"Characterization of an OprL null mutant of Pseudomonas putida.";

J. Bacteriol. 178:5836-5840 (1996).

EMBL; X74218; CAB50780.1; -...

PRINTS; PRO0624; HISTONEHS.

SEQUENCE 372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
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STR.0793.
Salmbnella typhi.
Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae;
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                          Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
52 KEYAAAEAKYKAEA----AKKAYKAEAAKAAA---KEAAYEA 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Kappe S.H.I., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.

"A family of chimeric erythrocyte binding proteins of malar parasites."

Parasites."

Proc. Natl. Acad. Sci. U.S.A. 95:1230-1235(1998).

EMBL; AF031886; AAC05366.1; -.

SEQUENCE 1701 AA; 199268 MW; EDA8E2DEFD87CE8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Indels
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.5%; Score 157.5; DB 1
54.8%; Pred. No. 9.3e-05;
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1 Similarity 53.5%; Pred. No. 0.00048;
53; Conservative 9; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:848-852 (2001).
EMBL, AL627269, CAD05209.1; -.
PRINTS; PR00309; ANTIFREEZEI.
PRINTS; PR01574; TUBBYPROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Conservative
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Best Local Similarity
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                                             SEQUENCE FROM N.A.
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NCBI_TaxID=601;
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Mesorhizobium loti.
                                                                                                  Local Similarity
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SEQUENCE FROM N.A.
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01-NOV-1996
01-MAR-2002
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039576
1D 03957
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AC 03957
DT 01-M
DT 01-M
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GN CH1
OS ELMAN
OC ELMAN
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X MEDLINE=21156231; PubMed=11258796;

A Hayashi T. Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

A Hayashi T. Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Han G., Shiba T., Hattori M., Shinagawa H.;

A Kuhara S., Shiba T., Hattori M., Shinagawa H.;

T "Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 811-22(2001).

R EMBL; AR005552; AAG55075.1; -.

R FMBL; AR00308; ANTIFREEZEI.

R PRINTS; PRO0308; ANTIFREEZEI.

W Complete proteome.

W SEQUENCE 394 AA; 40517 MW; 5B58D3BEB230BDE28 CRC64;
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                                                                                                                                                                                                                           STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Membrane spanning protein, required for outer membrane integrity
(Membrane spanning protein TolA).
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Pectobacterium.
NCBI_TaxID=556;
                                                                                                                                                   Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
Escherichia
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Last annotation update)
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53.1%; Pred. No. 0.00015;
ive 6; Mismatches 23;
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                              394 AA
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                              PRT;
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                              PRELIMINARY;
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Best Local Similarity
Matches 51; Conserv
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                              Q8X965
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RESULT 6
0937K4
1D 0937K1
AC 0937I
DT 01-DD
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DE TOIA,
CO BECK
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RN [1]
RR SEQUIR
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1177 ÁBELRQQEBÁARLKÁBADÁKAKÁBÁBÁQAQÁBÁBAKAQÁBÁBAKÁKADABAKÁBABAKAK 1236
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                                                                                                                                                                                                                                                                                                                                                        1 AKKYAK---KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEKKYAKAKEKKEYAAA 57
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Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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Phyllobacteriaceae; Mesorhizobium.
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                                      genes.";
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                                                                                                                                                                                         Length 395;
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Ray M.C., Vianney A., Cotte-pattat N., Lazzaroni J.; "characterization of the Erwinia chrysanthemi tol.pal ge
Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ297885; CAC82708.1;
                                                                                                                        395 AA; 41601 MW; 3C0C1DC12E181013 CRC64;
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1-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein mill1482.
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Last sequence update)
Last annotation update)
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53.3%; Pred. No. 0.00018;
tive 13; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            EAKYK-AEAAKKAYKAEAAK----AAAKEAA 83
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EMBL, AP002997; BAB48847.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 1341 AA, 138670 MW, 79C5DB3
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(TrEMBLrel. 20, I
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RESULT 9 Q9CM70

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MEDINE=21470413; PubMed=11586360;
Parkhil J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebainia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamiln N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C. F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Yersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAKKAEKAAKKAEA--KAYKAAEAKKKAKAEAKKYA----KAAKAEKKEY 54
                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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"Evolutionary relationships of conserved cysteine-rich motifs adhesive molecules of malaria parasites.";
Mol. Biol. Evol. 0:0-0(2002).
EMBL, AY042083; AAL105081.1;
SEQUENCE 1866 AA; 212420 MW; DC692D7CFAE7D93F CRC64;
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NCBI_TaxID=5855;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81447B04B30A7E7C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 ------YAAAEAKYKAEAAKK-AYKAEAAKAAAKEAA 83
                01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.1%; Score 147.5; DB 10
45.2%; Pred. No. 0.00054;
cive 9; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 A-AAEAKYKAEAAKK---AYKAEAAKAAAKEAAYEA 86
                                                                          Tola colicin import membrane protein.
TOLA OR YPO1123.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AJ414146; CAC89966.1; -.
InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
                                                                                                                                                                                                                                           / BIOVAR ORIENTALIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388 AA; 40424 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Matches 47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:523-527
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=SALVADOR;
                                                                                                                        Yersinia pestis.
                                                                                                                                                                                NCBI_TaxID=632;
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01-JUN-2002
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                Yersinia
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Q8T5C8
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                                                    MEDILINE=96120862; PubMed=8590479;

Rebry S., Muller K., Lindauer A., Park P.B., Cornelius T., Schmitt R.;
T'He organization structure and regulatory elements of Chlamydomonas
T histone genes reveal features linking plant and animal genes.";
Curr. Genet. 28:333-345(1995).
R EMBL; U16726; AAA98452.1; -.
R EMBL; U16726; AAA98452.1; -.
R InterPro; IPR001386; Histone H1/H5.
R InterPro; IPR001386; Histone H1/H5.
R Pfam; PF00538; Linker histone; I.
R ProDom; PD000373; Linkerhist. N.
R SMART; SM00526; H15; 1.
C SEQUENCE 232 AA; 24693 MW; 2D006AE44ABFA037 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 KPKAAKPAKKTPTKKAAAKPKAEKKPKAAAKPKAEKKPKAAKPKAEKKAKAAKPAAKKSA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 AKKAATPKKAAAPKKEGAVKKTKAPKKEGEKKPKSAKKAEKKPKKEGEKKKAAKPAKAEK 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KKYAKKEKAYAKKAEKAAK-KAEAKAYKAA-----EAKKKAKAKAEAKKYAKAE-- 50
                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKEKAYAKKAEKAAKKAEA-----KAYKAAEAKKKAKAEAKKYAKAAEA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V., "Complete genomic sequence of Pasteurella multocida Pm70."; proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL, AE006136; AAK03052.1; -. HSSP; P19934; ITOL.
                                                                                                                                                                                                                                                                                                                                                                                37;
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                                                                                                                                                                                                                                                                                                                                        Score 148.5; DB 10; Length 232;
Pred. No. 0.00028;
7; Mismatches 29; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, gamma subdivision, Pasteurellaceae,
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47.2%; Pred. No. 0.0005;
ive 11; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 -----KKEYAAAEAKYKAEAAK-----KAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389 AA; 42197 MW; B4032F2A2FD9E94B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                            36.3%;
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01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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NCBI_TaxID=3055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PM70;
                                                                                                                                                                                                                                                                                                                                                                                  47;
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Best Local 5
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4

Matches

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EMBL; AF255740; AAK66966.1; -.
InterPro; IPR001386; Histone H1/H5.
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093946;
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                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 AKKAAPAKKAAVKKVAAKKAPAAKKAAVKKVAAKKAAPAKKAAVKKVAAKKAPAAKKAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanôsoma cruzi.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Welssenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, beta subdivision, Ralstonia group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 34.0%; Score 139; DB 16; Length 20
1 Similarity 52.6%; Pred. No. 0.0012;
50; Conservative 5; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 AA; 19279 MW; D3831B590510272D CRC64;
                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last sequence update)
Last annotation update)
128 ККАРААК---КАРААККАААКРААКРААКРА
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                                                                                                                                                200 AA
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Mol. Biochem. Parasitol. 57:317-330(1993)
EMBL; L04603; AAA96494.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004089; Chmtaxis transd.
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                           Created)
                                                                                                                                                PRT;
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InterPro; IPR000104; Antifreeze_1.
InterPro; IPR003993; treacle.
PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01503; TREACLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                 Probable histone H1 protein. RSC2793 OR RS00453.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=GMI1000;
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                                                                                                                                                                                                                                                                                                                                                                  Ralstonia.
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0C 02694
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Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae; Bufo.
NCBI_TaxID=30331;
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                                                                                                                                                 5; Gaps
                                                                                                                                                                                                            1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.

Kaiser B., Kunkel W., Saluz H.P., Munder T.;

"Identification of Candid albicans protein domains with
transcriptional activating properties in Saccharomyces cerevisiae.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

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                                                                                           Length 1128;
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"Two Functional Toad Histone H2A Genes Contain Different Core
Promoters: the TATA Box or the Inr Blement.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.9%; Score 134.5; DB.3; Length 212; Best Local Similarity 46.2%; Pred. No. 0.0028; Matches 37; Conservative 10; Mismatches 26; Indels 7
                                                                                                                                                 Indels
PROSITE; PS00294; PRENYLATION; UNKNOWN 1.
SEQUENCE 1128 AA; 119686 MW; 7997745D32B83656 CRC64;
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Last annotation update)
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Last annotation update)
                                                                                     Query Match 33.6%; Score 137.5; DB 5; Best Local Similarity 48.9%; Pred. No. 0.0086; Matches 43; Conservative 11; Mismatches 29;
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01-JUN-2002 (TrEMBLrel. 21,
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Pfam; PF00538; linker histone; 1.
PRINTS; PR01574; TUBBYPROTEIN.
SEQUENCE 224 AA; 22546 MW; 6DCA43441F4ABB2E CRC64;
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224;		9;
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Score 131.5; DB 13;		9; Mismatches
32.2%;	47.78;	ative
tch	Best Local Similarity 47.7%;	42; Conserva
Query Mai	Best Loca	Matches

<sup>6 6 6</sup> 

Search completed: March 10, 2003, 12:25:58 Job time : 46.5401 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 10, 2003, 12:15:01; Search time 44.8143 Seconds (without alignments) 255.712 Million cell updates/sec

US-09-816-989A-6

score:

1 AKKYAKKEKAYAKKAEKAAK..........KAYKAEAAKAAAKEAAYEA 86 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	268	65.5	99	21	AAY82574	Copolymer molecula
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60	156	38.1	100	21	AAY98499	Peptide #10 used i
0	156	38.1		21	AAY59044	Amino acid polymer
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# ALIGNMENTS

AAY82576 standard; peptide; 86 AA 28-JUL-2000 (first entry) AAY82576; 

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopethic; immunosuppressive; antithyroid; antiinflammatory; antiidabetic; thyromimetic; haemostatic; antiinflammator; thyromimetic; demostatic; antiinflammatory condition; multiple sclerosis; rheumatoid arthritis; inflammatory condition; multiple sclerosis; heumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; draves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus

Unidentified

WO200018794-A1

06-APR-2000

99WO-US22402. 24-SEP-1999; 98US-0101693. 25-SEP-1998; (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

CO LTD

(YEDA ) YEDA RES & DEV CO LI (TEVA-) TEVA PHARM USA INC.

WPI; 2000-317499/27.

Gad A,

98US-0101693. 99WO-US22402.

24-SEP-1999; 25-SEP-1998;

06-APR-2000.

Claim 10; Page 14; 72pp; English.

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune becompositis, autoimmune thyroiditis, autoimmune vecetinits, contact sensitivity disease, diabetes mellitus, Graves disease, Gulliain-Barre's syndrome, Hashimcto's disease, idiopathic myxoedema, myasthenia gravis, psyndrome, Hashimcto's disease, idiopathic myxoedema, myasthenia gravis, psyndrome, pempigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-shost disease, and delayed-type hypersenaitivity. The polypeptides of the invention have defined molecular weights and phylacial properties which are analogous to molecular melayer.
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                                                                                                                   Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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                                                                                                                                                                                            Claim 10; Page 14; 72pp; English
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AAY92571 to AAY92577 represent specifically claimed copolymer molecular weight TV-marker polypeptides (I) for determining the molecular weight to describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for CP polypeptides of the invention are used as molecular weight markers for CP glatiramer acetate related tetrapolymers. The polypeptides may also be used for treated preventing immune diseases in a mammal. Autoimmune CP diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple collections, autoimmune ophoritis, osteoarthritis, autoimmune to sclerosis, theumatoid arthritis, osteoarthritis, autoimmune cophoritis, autoimmune thyroiditis, autoimmune cophoritis, context sensitivity disease, diabetes mellitus, carves disease, duillain-Barre's syndrome, Hashimoto's disease, idiopathic comparated molecular weightes and physical properties which are analogous to continue molecular weightes and physical properties which are analogous to continue molecular weightes and physical properties which are analogous to continue molecular weightes and physical properties analogous to continue molecular mellinum continum continum continum continument continued continument continument continument continument continument continument continument continument continume
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copolymer; molecular weight marker; TV-marker; immune disease;
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89.5%; Pred. No. 4...
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pemphigus vulgaris; systemic lupus erythematosus

WO200018794-A1 Unidentified

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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and amino acid composition corresponding to the copolymer. The polypeptides markers for glatiramer acctate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatorid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune vecetinits, contact sensitivity disease, diabetes mellitus, Graves purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Gullain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psyndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic collis, contact sensitivity disease, while are a syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic collis, contact sensitivity disease which can be treated include by the contact sensitivity disease, diabetes mellitus, Cromator sensitivity disease, diabetes mellitus, or systemic lugar erythemetogus Mediated emediated diseases which can be treated include the contact sensitivity disease which can be treated include the contact sensitivity disease which can be treated include the contact sensitivity disease which can be treated include the contact sensitivity disease which can be treated the contact sensitivity disease.
inflammatory condition; multiple sclerosis; rheumatoid arthritis; cothn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensityity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                        pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                           99WO-US22402.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-317499/27.
                                                                                                                                                                                                                                        WO200018794-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lis D;
                                                                                                                                                                                                                                                                                                                                                           24-SEP-1999;
                                                                                                                                                                                                                                                                                                06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gad A,
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5
                                                                Gaps
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                                                                                                                         1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEA 60
                                                            27;
                               DB 21; Length 109;
                                                                                                                                                                                    61 YKAEAKKYAKAAKAEKKEYAAAEAK-KAEAA-KAYKAEAAKAAAKEAAYEA 109
                                                            Indels
                                                                                                                                                       37 -KAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAAKEA
                                                            3;
                             Score 312.5; DB
Pred. No. 2e-21;
1; Mismatches
                             76.48;
                                            Best Local Similarity 72.1
Matches 80; Conservative
                                          Similarity
109 AA;
Sequence
                             Query Match
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AAY82574 standard; peptide; 66
                           AAY82574;
AAY82574
ID AAY8
XX
AC AAY8
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Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; antiposoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; chronic immune thrombocytopaenia purpura, colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                      Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                        Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                 99WO-US22402.
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(first entry)
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                                                                                                                                                                                                               WO200018794-A1.
                                                                                                                                                                                                                                                                                                                                                     Gad A, Lis D;
                                                                                                                                                                                                                                                                 24-SEP-1999;
                                                                                                                                                                                                                                                                                        25-SEP-1998;
 28-JUL-2000
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Weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune hyproidatis, autoimmune mammal and an ammune planting than an ammune and ammune and an ammune and an ammune and an ammune and an ammune an uveoretinitis, Crohn's disease, chronic immune thrombocytopeenia uveoretinitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as

65.5%; Score 268; DB 21; Length 66; Pred. No. 1.3e-17; 0; Mismatches 75.6%; Conservative Local Similarity 66 AA; 65; Sequence Query Match Matches

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20; Gaps

1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAKAEKEKEYAAAEAK 60

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Ouery Match 57.0%; Score 233; DB 21; Length 56;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uveoretinitis, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, Crohn's disease, chronic immune thrombocytopaenia disease, cuillain-Barre's syndrome, Haahimoro's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acette molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                 Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinfiammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidabetic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Gulllain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                   Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.
  ----YKAEAAKAAAKEAAYEA 66
                                                                                                                              AAY82573 standard; peptide; 56 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 14; 72pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200018794-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3ad A, Lis D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-1998;
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                                                                                                                                                                                  AAY82573;
  20
                                                                                                 AAX82573
AAX8257
AA
                                                                           RESULT 5
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To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20.NOV-1948 US469100), NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences.

A methionine residue occurs between the Protein A and rCOP-1 sequences, originaling from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein.

C COP-1-77 contains oligonucleotide duplexes incoding the following segments: YKK, BER, KAK, And AAA. The N-terminal alanine residue is left behind following CNP releaved of the fusion protein.

The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                 1,
                                    30; Gaps
                                                                                         1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autolmmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 163; DB 11; Length 154; Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing genes encoding random polymers of aminoacid(s) - i
producing recombinant polypeptide(s) with biological and/or
immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant copolymer 1-77, myelin basic protein analogue
                                 Indels
62.8%; Pred. No. 1.6e-14;
ive 2; Mismatches 0;
                                                                                                                                                        1 AKKYAKKEKAYAKKAEKAKKAEAKAYKAAEAKKKAEAK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR06445 standard; protein; 154 AA
                                                                                                                                                                                                                           61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                       40 -----YKAEAAKAAKEAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 11; 25pp; English.
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42.3%;
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89US-0312541.
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                                 54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1990-255848/34.
N-PSDB; AAQ05664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR06445;
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                                 Matches
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Length 106;

106 AA;

Sequence

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                                                                                                                  Gaps
                                       ----- 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control sdemyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity
                                                                                                                                                                                                                                                                                                                                                                                 Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                         Recombinant copolymer 1-19, myelin basic protein analogue.
            Indels
          20;
         9; Mismatches
                                                                                                  41 ---KKYAKAAKAEKKEYAAAEAKYKAEA----
                                                                                                                                                                                                                                                                  AAR06446 standard; protein; 106 AA.
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89US-0312541.
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         55; Conservative
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See also AAQ05664.
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                                                                                                                                                                                        132 AEKAKEAEYK 141
                                                                                                                                                            79 ---AKEAAYE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ06446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-1990;
17-FEB-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                              AAR06446;
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Matches
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The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36613-A36652 and peptide sequences AAY36456-Y98500 are used in the construction of the transporter system of the invention. The ransporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g. for treating cardiovascular disease, cancer, and infection. The cransporter systems are also used to create transgenic animals (as models for human carcinogenesis or disease or for drug testing). Other uses include transforming cells or produce proteins, or transfecting cells in clude transforming cells to produce proteins, or transfecting cells in ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from endosomes, without requiring endosomal or lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent
                                          Gaps
                                                                                                 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEK-----KE 53
                                                                                                                                                                                                                                                                                                                                                                                                                              Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith LC;
                                        20; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Peptide #10 used in nucleic acid transporter system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WOO SLC,
 Score 157; DB 11;
Pred. No. 2.4e-07;
9; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Column 125-128; 108pp; English
                                                                                                                                                     54 YAAAEAKYKAEAAKKAYKAEAAKAAAKEAAYE 85
                                                                                                                                                                        Gottchalk S, Sparrow J, Cristiano RJ,
                                                                                                                                                                                                                                                                                   Ą.
                                                                                                                                                                                                                                                                                 AAY98499 standard; Peptide; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BAYU ) BAYLOR COLLEGE MEDICINE.
   38.4%;
55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0167641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93WO-US02725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-0855389
                                                                                                                                                                                                                                                                                                                                                       31-JUL-2000 (first entry)
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-281993/24.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6033884-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAR-2000.
                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                   AAY98499;
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                                          Matches
                                                                                                                                                                                                                                            RESULT 8
AAY98499
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Gaps

5,

Indels

30;

6; Mismatches

86

Length 100;

DB 21;

Score 156; DB 21 Pred. No. 2.7e-07

38.1%; 55.3%;

100 AA;

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1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                                                                                                                                                                                    59 AKYKAEAAKKAYKAEAAKAAAKEAA 83
                                                                                                                                                                                                                                                                                             AKAKAKAKAKAKAKAKAKA
                                                                                                                 47; Conservative
                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU04289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                         AAU04289
      X S
                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognises and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through cytosis; (c) a nucleic complex or (e) a lysis moiety that enables the transport of the entire complex or (e) a lysis moiety that enables the transport of the entire complex or from the cell surface directly into the cytoplasm of the cell. The NTS call into the cytoplasm of the cell. The NTS call into the cytoplasm of the cell as the nucleus of specific cells. The NTS can be used to treat disorders by targeting transgenic animals for assessing human disease, such as cancer, in an example of the coll of various nucleic acide to be studied by targeting specific expression into specifically targeted tissue culture cells. The Collysis and services of specific expression into specifically targeted tissue culture cells. The collysis agent within the NTS avoids the problem of endosomal/lysosomal
                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Lys-Ala in positions 3 to 100 may be optionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                              Gaps
                                                                     1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                                                                                               cytosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nuclear membrane, lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer.
                           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith LC;
    Pred. No. 2.7e-07;
6; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid polymer seq ID NO: 64 of US5994109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Columns 123-124; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cristiano RJ, Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    AAY59044 standard; peptide; 100 AA
                                                                                                                                                           59 AKYKAEAAKKAYKAEAAKAAKEAA 83
                                                                                                                                                                                       62 AKAKAKAKAKAKAKAKAKAKA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      absent '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0167641.
92US-0855389.
93WO-US02725.
93US-0167641.
55.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0460890.
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                           47; Conservative
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-038262/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BAYU ) BAYLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-1992;
19-MAR-1993;
14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                AAY59044;
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XXX AAYS
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                                                                                                                                                                                                    Nucleic acid transport, cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                           /note= "Lys-Ala in positions 3-100 may be present or absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid transport system, useful for creating transgenic for assessing human disease such as cancer in an animal model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۵,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sparrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                        Poly-Lys-Ala used in nucleic acid transporter system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.1%; Score 156; DB 22;
55.3%; Pred. No. 2.7e-07;
iive 6; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gottchalk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Column 131, 111pp; English
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 3..100
AAU04289 standard; Peptide; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92US-0855389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-0167641
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-365933/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 AA;
                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6177554-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1993;
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                                                                                                       23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JAN-2001,
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59 AKYKAEAAKKAYKAEAAKAAAKEAA 83

62

M. tuberculosis histone H1-like antigen.

23-NOV-1999 (first entry)

AAY34055;

Mycobacterium tuberculosis.

WO9945955-A1 16-SEP-1999.

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Ulcerative colitis; histone; H1-like antigen; porin antigen;
Bacteroides antigen; inflammatory bowel disease; IBD; pANCA; diagnosis;
perinuclear anti-neutrophil cytoplasmic antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of histone H1, porin or Bacteroides antigens as targets for the diagnosis, prevention and treatment of ulcerative colitis
                                                                                                                                                                   AAY34055 standard; protein; 214 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can system can be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, such subpressors, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems.
                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen; bacterial antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel system (I) for delivering a nucleic acid
                   28
                                  Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                 1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.1%; Score 156; DB 22; Length 100; 55.3%; Pred. No. 2.7e-07; ive 6; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                    Nucleic acid transporter system peptide ligand SEQ ID NO 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WOO SLC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Column 125-126; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cristiano RJ,
                                                                                                                                                                                                                       AAB45852 standard; Protein; 100 AA
                                                                                         83
                                                                                                                              86
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                                                                                                              59 AKYKAEAAKKAYKAEAAKAAAKEAA
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                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 55.3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gottchalk S, Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-049093/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-DEC-1993;
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                                                                                                                                                                                                                                                                                                 21-MAR-2001
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                                                                                                                                                                                                                                                            AAB45852;
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                                                                                                                            62
                                                                                                                                                                                                      AAB45852
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Claim 2; Fig 11; 134pp; English.

98US-0041889. 99WO-US05492

12-MAR-1999; 12-MAR-1998; (REGC ) UNIV CALIFORNIA.

WPI; 1999-551215/46. Braun J, Cohavy O;

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The invention provides a method for the diagnosis, prevention and treatment of ulcerative colitis (UC) using histone H1-like antigen, a portion antigen or a Bacteroides antigen as a target antigen. The novel method of diagnosing UC in a subject suspected of having inflammatory bowel disease (IBD) comprises: (1) obtaining a sample from the subject; (2) contacting the sample with a histone H1-like antigen, or perinnclear anti-neutrophil cytoplasmic antibody (PANCA)-reactive fragment, to form a complex of the histone H1-like antigen, and (3) detecting the resence or absence of the complex; where the presence of the complex indicates that the subject has UC. The pANCA-reactive histone H1-like in the antigen, porin antigen and Bacteroides antigen are useful in the antigen, prevention and treatment of UC. The methods can also be used for identifying agents useful for treating UC. The present sequence represents a M. tuberculosis histone H1-like antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKAKAEAKKYAKAAKAEKKEY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.9%; Score 147; DB 20; Length 214; 50.0%; Pred. No. 4.1e-06; tive 3; Mismatches 34; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 TKAVKKTAVKASVRKAATKAPAKKAAKRPATKA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 AAAEAK--YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 AA;
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1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58

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such as tuberculosis
                                                                                                                                                                                     Yamada T, Matsumoto
                                                                                                                                         (SAKA ) OTSUKA PHARM
(YAMA/) YAMADA T.
(MATS/) MATSUMOTO S.
                               Mycobacterium bovis
                                                                                                                                                                                                          WPI; 2000-543393/49
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma cruzi.
                                                                                                                                                                                                                     N-PSDB; AAA88001
                                                     WO200044905-A1
                                                                                                                      29-JAN-1999;
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                                                                            03-AUG-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR84569;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Region
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR84569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٠,
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                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides a method for diagnosing ulcerative colitis in a subject suspected of having inflammatory bowel disease. The method comprises reacting a patient sample with a porin antigen that is immunologically reactive with pANCA (perinclear anti-neutrophil cytoplasmic antibodies) and detecting formation of a Ag-pANCA complex as indicative of ulcerative colitis. The method is used to diagnose ulcerative colitis or susceptibility to it. The present sequence represents a histone H1-like protein of M. tuberculosis, designated 214.
                                                                                                                                                                                                                                                                                                                                        Diagnosing ulcerative colitis or susceptibility, by detecting complex formation between microbial porin antigen and perinuclear anti-neutrophil cytoplasmic autoantibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 AKKVAK--KAPAKKATKAAKKAATKAPAKKAATKAPAKKAATKAPAKKAVKATKSPAKKV 168
                                                                                                          Ulcerative colitis; inflammatory bowel disease; porin antigen; MAb;
pANCA; perinuclear anti-neutrophil cytoplasmic antibody; 214 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium bovis BCG strain; mycobacterium DNA binding protein 1; MDP1; slcw growing acid-fast bacterium protein; immunogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKAKAEAKKYAKAAKAEKKEY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 147; DB 21; Length 214;
Pred. No. 4.1e-06;
3; Mismatches 34; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mydobacterium bovis BCG strain MDP1 protein SEQ ID NO:2.
                                                                                     M. tuberculosis histone H1-like protein, 214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 TKAVKKTAVKASVRKAATKAPAKKAAKKAATKA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 AAAEAK--YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                    AAY57353 standard; Protein; 214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä.
                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Fig 10; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB20575 standard; Protein; 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.9%;
                                                                                                                                                                                                                    98US-0041889
                                                                                                                                                                                                                                          96US-0057846
                                                                                                                                                                                                                                                   97US-0837058
                                                                                                                                                     Mycobacterium tuberculosis.
                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Conservative
                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA.
                                                                                                                                histone H1; isoform.
                                                                                                                                                                                                                                                                                                                   WPI; 2000-255695/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                               Braun J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 AA;
                                                                                                                                                                                                                    12-MAR-1998;
                                                                                                                                                                                                                                        12-APR-1996;
                                                               13-JUN-2000
                                                                                                                                                                                                                                                    11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-2000
                                                                                                                                                                         US6033864-A
                                                                                                                                                                                              07-MAR-2000
                                                                                                                                                                                                                                                                                               Cohavy 0,
                                           AAY57353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB20575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
RESULT 13
           AAY57353
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The present sequence represents the Mycobacterium bovis BCG strain mycobacterium DNA binding protein 1 (MDP1), which has immunogenicity against pathogenic acid-fast bacteria. The MDP1 protein can be used for diagnosis and treatment of diseases involving pathogenic acid-fast bacteria, such as tuberculosis, Mycobacterium avium intracellular complex (MAC) and Hansen's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Mycobacterium DNA binding protein 1 immunogenic for pathogenic acid-fast bacteria for diagnosis, treatment and prevention of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 AKKVAK--KAPAKKATKAAKKAATK----APAKKAATKAPAKKAVKATKSPAKKVTKAVK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKA-KAEAKKYAKAAKAAKAEKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241..450
/label= repeat_region
/note= "15 of 69 repeat units of 14 amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCR27; Chagas disease; repeat unit; diagnosis; blood screening; recombinant; fusion protein; glutathione-S-transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 205;
pathogenic acid-fast bacterium; diagnosis; tuberculosis; MAC;
Mycobacterium avium intracellular complex; Hansen's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.8%; Score 146.5; DB 21; 53.9%; Pred. No. 4.3e-06; tive 3; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma cruzi TCR27 polypeptide, Ag8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 KTAVKASVRKAATKAPAKKAAAKRPATKA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K--YKAEAAKKAYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR84569 standard; Protein; 472 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 2A; 62pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0022588.
                                                                                                                                                                                                                                                                                                                                   28-JAN-2000; 2000WO-JP00455.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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YAMADA T.
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AAR84565-R84569 are polypeptides of the TCR27 protein of T.cruzi
The proteins are all fusion products with glutathione-S-transferase
(GST) and some contain a linker sequence. The TCR27 protein comprises
a 95 amino acid (aa) N-terminal region; 69 repeats of a highly
conserved 14 as sequence, the Ag8 polypeptide contg. 15 of the 69
encodes the GST sequence, the Ag8 polypeptide contg. 15 of the 69
repeat units and also contains a linker sequence. The TCR27
polypeptides of the invention are useful for the diagnosis of Chagas
continuous and also contains a linker sequence. The TCR27
polypeptides of the invention are useful for the diagnosis of chagas
continuous antibodies; or for blood screening. The TCR27 protein
has epitopes to which meat T.cruzi infected individuals have
anti-T.cruzi antibodies; or for blood screening. The TCR27 protein
has epitopes to which meat T.cruzi infected individuals have
antibodies. The TCR27 polypeptides will not react with serum from
patients with leishmaniasis, schistosomiasis, or autoimmune disease
and are hence less likely to cause false positives in diagnosis.
                                                                                                                                                                                                                                                                                          New polypeptide(s) from the TCR27 protein of Trypanosoma cruzi - s
immunoassay reagent for specific diagnosis of Chagas disease, also
related nucleic acid and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 44-45; 68pp; English.
                       95WO-US03191.
                                                                  94US-0216894.
                                                                                                          (KIRC/) KIRCHHOFF L V. (OTSU/) OTSU K.
                                                                                                                                                                             Kirchhoff LV, Otsu K;
                                                                                                                                                                                                                             WPI; 1995-344618/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 472 AA;
                                                                                                                                                                                                                                                N-PSDB; AAT05333
                     20-MAR-1995;
                                                                  24-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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346 ATKVAEAEK---QKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEA 402 5; Gaps 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAK-AEKKEYAAAEA 59 33.6%; Score 137.5; DB 16; Length 472; ilarity 48.9%; Pred. No. 6.9e-05; Conservative 11; Mismatches 29; Indels 5; Best Local Similarity Matches 43; Conserva 임 8

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Search completed: March 10, 2003, 12:21:30 Job time : 44.8143 secs

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GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

Run on:

US-09-816-989A-6

1 AKKYAKKEKAYAKKAEKAAK.......KAYKAEAAKAAAKEAAYEA 86 score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

188354 Total number of hits satisfying chosen parameters:

188354 seqs, 42170167 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

| Contact | Cont /prodata/1/pubpaa/USO9\_PUBCOMB.pep:\*/ptcodata/1/pubpaa/US10\_NEW\_PUB.pep:\*/ptcodata/1/pubpaa/US10\_PUBCOMB.pep:\* /grafic //prodata/1/pubpaa/USO9 PUBCOMD.pep: # /cgn2\_6/ptodata/1/pubpaa/USO9 PUBCOMD.pep: # /cgn2\_6/ptodata/1/pubpaa/USO9 USO USO PUBCOMD.pep: # /cgn2\_6/ptodata/1/pubpaa/USO0 NEW PUB.pep: # /cgn2\_6/ptodata/1/pubpaa/USO0 NEW PUB.pep: # /cgn2\_6/ptodata/1/pubpaa/USO0 PUBCOMB.pep: # /cgn2\_6/pto Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Sequence 6, Appli	Sequence 5, Appli	Sequence 7, Appli	Sequence 4, Appli	6	Seguence 8, Appli	Sequence 5, Appli	Sequence 201, App	Sequence 2, Appli	Sequence 27, Appl	Sequence 24, Appl	Sequence 95, Appl		Sequence 36182, A	Sequence 3, Appli	Seguence 5197, Ap	Sequence 1, Appli	Sequence 100, App	Sequence 10314, A
	ID	US-09-816-989A-6	US-09-816-989A-5	US-09-816-989A-7	US-09-816-989A-4	US-09-816-989A-3	US-09-820-843A-8	US-10-184-832-5	US-10-051-643-201	US-09-816-989A-2	US-09-820-843A-27	US-09-820-843A-24	US-09-820-843A-95	US-09-820-843A-23	US-09-864-761-36182	US-09-124-280A-3	US-09-738-626-5197	US-09-816-989A-1	US-09-919-497-100	US-09-815-242-10314
	DB	9	70	10	10	10	0	6	σ	10	δ	σ	0	0	10	10	σ	10	10	10
	Query Match Length DB	98	77	109	99	99	372	452	223	45	356	309	369	352	617	434	9	35	582	890
de	Ouery Match	100.0	85.9	76.4	65.5	57.0	34.7	32.0	31.7	30.9	30.1	28.4	27.5	27.0	27.0	26.7	26.5	26.4	26.4	26.2
	Score	409	351.5	312.5	268	233	142	131	129.5	126.5	123	116	112.5	110.5	110.5	109	108.5	108	108	107
	Result No.	н	7	3	4	2	y	7	80	6	10	11	12	13	14	15	16	17	18	19

Sequence 13765, A	Sequence 5298, Ap	Sequence 12294, A	Sequence 1, Appli	Sequence 46, Appl	Sequence 48, Appl	Sequence 90, Appl	Sequence 11216, A	Sequence 5198, Ap	Sequence 1164, Ap	Sequence 38, Appl	Sequence 37061, A	Sequence 5, Appli	Sequence 2, Appli	Sequence 559, App	Sequence 8, Appli	Sequence 8, Appli	Sequence 9, Appli	Sequence 5759, Ap	Sequence 12408, A	Sequence 5854, Ap	Sequence 7, Appli	Sequence 53, Appl	Sequence 51, Appl	~	Sequence 229, App
US-09-815-242-13765	US-09-815-242-5298	US-09-815-242-12294	US-09-882-774-1	US-09-999-724-46	US-09-999-724-48	US-09-999-724-90	US-09-815-242-11216	US-09-815-242-5198	US-09-925-300-1164	US-09-765-272-38	US-09-864-761-37061	US-10-093-892-5	US-09-923-304-2	US-09-925-302-559	US-09-985-442-8	US-09-983-580-8	US-10-093-892-9	US-09-815-242-5759	US-09-815-242-12408	US-09-738-626-5854	US-09-820-843A-7	US-09-883-825-53	US-09-883-825-51	US-09-971-536-69	US-10-002-344A-229
10	10	10	σ	0	σ	σ	10	10	10	10	10	σ	10	10	σ	10	σ	10	10	σ	თ	10	10	σ	σ
892	454	454	619	118	218	102	829	840	300	453	71	105	220	265	84	84	96	318	318	365	203	564	634	1463	16
26.2	25.6	25.6	25.4	25.2	25.2	24.9	24.3	24.3	23.2	23.1	22.9	22.4	22.2	22.2	22.0	22.0	22.0	22.0	22.0	22.0	21.8	21.5	21.5	21.4	21.3
107	104.5	104.5	104	103	103	102	99.5	99.5	95	94.5	93.5	91.5	91	91	90	06	90	90	90	90	89	88	88	87.5	87
20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

```
Sequence 6, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 409; DB 10; ilarity 100.0%; Pred. No. 2.5e-28; Conservative 0; Mismatches 0;
                                                                                                                                                                   THIE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PELING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3:1
SOFTWARE: Patentin version 3:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-816-989A-6
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1 AKKYAKKEKAYAKKAEKAAKKAEAAYAYKAABAKKKAKAKAKAKAAKKYAKAKAKKEKEYAAAEAK 60 61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86 RESULT 2 US-09-816-989A-5 ; Sequence 5, Application US/09816989A YKAEAAKKAYKAEAAKAAAKEAAYEA 61 g g ò

US20020115103A1

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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKTITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 927/US99/22402
PRIOR APPLICATION NUMBER: 927/US99/22402
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENT VERSION 3.1
SEQ ID NO 4
LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lis, Doris

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: ADD FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT FILING DATE: 2001-03-23

PRIOR PAPLICATION NUMBER: 60/101,693

PRIOR FILING DATE: 1998-09-25

PRIOR PAPLICATION NUMBER: PCT/US99/22402

PRIOR FILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.6%; Pred. No. 1.2e-16;
Matches 65; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 57.0%; Score 233; DB 10; 1 Similarity 62.8%; Pred. No. 9e-14; 54; Conservative 2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 -----YKAEAAKAAKEAAYEA 66
                                                                                Sequence 4, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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SEQ ID NO 3
LENGTH: 56
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Gad, Alexander
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 54; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-816-989A-3
                                                           US-09-816-989A-4
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; Sequence 7, Application US/09816989A
; Patent No. US20020115103A1
; GENERAL INFORMATION:
    APPLICANT: dat, Alexandex
; APPLICANT: dat, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; TILLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT PILING DATE: 1998-09-25
; PRIOR PILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO? 7
GENERAL INFORMATION:

APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Daria
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/6100-A-PCT-US
CURRENT PELLING DATE: 2001-03-23
PRIOR PELLING DATE: 2001-03-25
PRIOR PILLING DATE: 1998-09-25
PRIOR PILLING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTMARE: PRECHIN VEXESON 3.1
SEQ ID NO 5
LENGTHE: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 АККУАККЕКАУАККАЕКААККАЕАКАУКААЕАККАКАКАЕАККУАКАЕККЕУАААЕАК 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.9%; Score 351.5; DB 10; Length ilarity 89.5%; Pred. No. 1.5e-23; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-816-989A-7
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Best Local Si
Matches 80;
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: US/09/816,989A
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Version 3.1
SEQ ID NO. 2
                                                                                                                                                                                                                                            APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L. J.

APPLICANT: Tan, Paul L. J.

APPLICANT: Tan, Paul L. J.

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: OSystem using Mycobacterium Vaccae

FILE REFERENCE: 11000.1008c2

CURRENT PALION DATE: 2002-01-18

PRIOR PLILING DATE: 1998-09-17

PRIOR FILING DATE: 1999-09-17

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 208

SEQ ID NO 201

LENGTH: 223
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKK---EKAYAKKAEKAAKKAEAK--AYKAAEAKKKAKAEAKKYAKAAKAEKKEYA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.7%; Score 129.5; DB 9; Best Local Similarity 54.3%; Pred. No. 0.00018; Matches 50; Conservative 5; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 AAEAKYKAEAAKKAYK-AEAAKAAAKEAAYEA 86
                                                                                                                                                                            Sequence 201, Application US/10051643
Publication No. US20020197265A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09816989A, Patent No. US20020115103A1, GENERAL INFORMATION: APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Mycobacterium vaccae US-10-051-643-201
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ORGANISM: Artificial Sequence
                                                     153 KAEAKAEAKAEAKE 166
     68 KAYKAEAAKAAAKE 81
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US-09-816-989A-2
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Publication No. US20030039963A1
GENERAL INFORMATION:
APPLICAMY: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEUL AS ANTI-INFECTIVES
FILE REFERENCE: Q65915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/10184832

Sequence 5, Application US/10184832

Publication No US20030022857A1

GENERAL INFORMATION:

APPLICANT: Xu et al.

TITLE OF INVENTION: COMPOSITIONS AND WEIGHT DISORDERS, INCLUDING OBESITY

FILE REFERENCE: MPI2001-056P1NM

CURRENT APPLICATION NUMBER: US/10/184,832

CURRENT FILING DATE: 2002-06-28

PRIOR FILING DATE: 2001-07-05

PRIOR FILING DATE: 2001-07-05

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYA-----KKEKAYAKKAEKAAKK----AEAKAYKAAEAKKKAKAEAKKYAKAAKAEK 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 34.7%; Score 142; DB 9; Length 372; Best Local Similarity 52.1%; Pred. No. 2.8e-05; Matches 49; Conservative 9; Mismatches 22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
CTHER INFORMATION: outer membrane integrity protein (tolA)
NAME/KEY: misc feature
CTHER INFORMATION: gi|1573353
US-09-820-843A-8
1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 KAKAAAEAKAKADAEAKA--ATEAKRKADQASLD 246
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                                                                                   -----YKAEAAKAAAKEAAYEA 56
                                                     61 YKAEAAKKAYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: H. influenzae
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; ORGANISM: Mus musculus
US-10-184-832-5
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Best Local Similarity
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                                                                                                                                                                              RESULT 6
US-09-820-843A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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Sequence 95, Application US/09820843A
Publication No. US20030039963A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Council Of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      % Sequence 23, Application US/08920843A

problication No. US20030039963A1

problication No. US20030039963A1

problication No. US20030039963A1

problication No. US20030039963A1

problication No. US2003003963A1

prints of invention: A compurational method for the identification of candidate professional method for the invention: USEPUL AS ANTI-INFECTIVES

prints of invention: USEPUL AS ANTI-INFECTIVES

prints despite the invention Number: US/09/820,843A

current APPLICATION NUMBER: US/09/820,843A

prints of SEQ ID NOS: 118

problem 13.0

problem 23

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problem 23.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
27.5%; Score 112.5; DB 9; Length
Best Local Similarity 38.8%; Pred. No. 0.0081;
Matches 33; Conservative 18; Mismatches 27; Indels
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CTHER INFORMATION: alginate regulatory protein AlgP
NAME/KEY: misc_feature
NAME/KEY: misc_feature
US-09-820-8430-834-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature

) OTHER INFORMATION: conserved hypothetical protein

) NAME/KEY: misc_feature

) OTHER INFORMATION: gi|3322751

US-09-820-843A-95
                                                                                                                                                                                      242 ААТААКРААКРААКРААККРААККРААКРААКРАА 277
                                                                                                                                       55 AAAEAKYKAE-AAKKAYKAEAAK-----AAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 RRKEAEEARRKEAEEARRKEAEFEA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 ----AKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 369
TYPE: PRT
ORGANISM: T. pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                    RESULT 12
US-09-820-843A-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REPREBUCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEITINE OF INVENTION: USEFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
THE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 24
LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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Pred. No. 0.0034;
1; Mismatches 35; Indels 14; Gaps
1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAYAKKA-----EKAAKKA-----EAKAYKAAEAKKKAKAKAK 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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) OTHER INFORMATION: polyhydroxyalkanoate synthesis protein PhaF

; NAME/KEY: misc_feature

) OTHER INFORMATION: gi|9951352

US-09-820-843A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.1%; Score 123; DB 9; Length 356;
42.6%; Pred. No. 0.001;
Live 13; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 AKREKEVAAKAEQERLAKEKAAKEAADKAKKEKERAAKAEAERKAQEA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 AKAEKKEYAAAE----AKYKA--EAAKKAYKAE--AAKAAAKEAAYEA 86
                                                    1 AKKYAKK-----AKAEKA----KKAYKAAEAKKAAKYE-
                                                                                                                                                                                                                                                                                          Sequence 27, Application US/09820843A Publication No. US20030039963A1 GENERAL INFORMATION:
                                                                                                                                       US-09-820-843A-24
; Sequence 24, Application US/09820843A
; Publication No. US20030039963A1
; CENERAL INFORMATION:
                                                                                                         61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
OTHER INFORMATION: tolA protein
NAME/KEY: misc feature
OTHER INFORMATION: g1|955354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 28.4%;
l Similarity 47.9%;
40; Conservative 1
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Best Local Similarity 42.6*
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                        RESULT 10
US-09-820-843A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-820-843A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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Sequence 1. Application US/09124280A
Patent No. US20020034520A1
GENERAL INFORMATION:
APPLICANT: POTTO, Massimo
TITLE OF INVENTION: NEGATIVE BACTERIAL INFECTIONS AND ENDOTOXIN RELATED DISEASES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hedman, Gibson & Costigan
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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0
                                                                                                                                                                            DB 10; Length 617;
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
INFORMATION: EXPRESSED IN BALLIN, SIGNAL = 5.6
INFORMATION: SWISSPROT HIT: P12036, EVALUE 2.00e-33
INFORMATION: EST_HUMAN HIT: BF445754.1, EVALUE 3.00e-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.7%; Score 109; DB 10; Length 434; 36.2%; Pred. No. 0.019; Live 11; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette, 3.50 inch, 1.44 Mb storage
                                                                                                                                                                         27.0%; Score 110.5; DB 10; 39.0%; Pred. No. 0.021; tive 10; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COSTIGAT, James V.
REGISTRATION NUMBER: 576-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 302-8989
TELEPAX: (212) 302-8989
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,280A
FILING DATE: July 29,1998
                                                                                                                                                                                                                                                                                                                                                                                                                                            62 KAEAAKKAYKAEAAKAAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 KKKKKKKKKKKKKKKK 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 KAEAAKKAYKAEAAKAAKE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 36.2%;
Matches 29; Conservative
                                                                                                                                                                                                       Best Local Similarity 39.0% Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 434 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
: USA
OTHER INFORMATION: I OTHER INFORMATION: S OTHER INFORMATION: S OTHER INFORMATION: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                 US-09-864-761-36182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-124-280A-3
                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
     Gaps
                                                                                                                    1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAKAEKKEYAAAEAK 60
        43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXPRESSED IN HELLA, SIGNAL = 1.3
EXPRESSED IN HELLOO, SIGNAL = 0.94
EXPRESSED IN HEART, SIGNAL = 1.3
EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 36182
LENGTH: 617
     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THILE REFERENCE: AGENIE ACTIVESTION ANALISES CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/01180,312
PRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-3
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
PRIOR APPLICATION NUMBER: US/09/83,366
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PLING DATE: 2001-01-30
PRIOR PURING DATE: 2001-01-30
                                                                                                                                                                                                                                     235 АКРААКРУАКРТАКРААКТАААКРААКРА 267
                                                                                                                                                                            61 YKAEA-----AKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                              Sequence 36182, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAP TO AC005529.7
     39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: M
OTHER INFORMATION: E
OTHER INFORMATION: E
OTHER INFORMATION: E
        Matches
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Search completed: March 10, 2003, 12:53:44 Job time : 25.7251 secs

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March 10, 2003, 12:15:04; Search time 15.2405 Seconds (without alignments) 166.029 Million cell updates/sec
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                   262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                     US-09-816-989A-6
409
                                                                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	156	38.1	100	. ~	US-08-460-890A-64	Sequence 64, Appl
7	156	38.1	100	m	US-08-167-641C-64	64,
e	156	38.1	100	4	US-08-460-971A-64	Sequence 64, Appl
4	156	38.1	100	4	US-08-462-040-64	64,
2	147	35.9	214	m	US-09-041-889-27	27,
9	۲.	33.6	472	7	US-08-216-894-10	10,
7	137.5	33.6	472	4	US-09-115-746-10	10
8	7	33.6	564	7	US-08-216-894-2	7
6	137.5	33.6	564	4	US-09-115-746-2	Sequence 2, Appli
10	7.	33.6	643	7	US-08-216-894-8	8
11	137.5	33.6	643	4	US-09-115-746-8	Sequence 8, Appli
12	133.5	32.6	433	Н	US-08-346-849-2	7
13	133.5	32.6	433	7	US-08-293-284A-2	α,
14	129.5	31.7	223	4	US-09-095-855-201	
15	129.5	31.7	223	4	US-09-205-426-201	201
16	127.5	31.2	1507	m	US-08-929-329-5	'n
17	127	31.1	222	٣	US-09-041-889-3	Sequence 3, Appli
18	127	31.1	222	m	US-08-837-058-3	m
19	121		158	ო	US-09-041-889-40	40,
20	121	29.6	226	ო	US-09-041-889-32	32,
21	119.5	29.5	26	4	US-08-993-008A-6	ý
22	117	28.6	218	ო	US-09-041-889-4	4,
23	117	28.6	218	m	US-08-837-058-4	4,
24	115.5	28.2	262	Н	US-08-403-379A-1	۲,
25		28.5	262	0	US-08-929-414-1	ų,
26	115.5	28.2	263	7	US-08-557-309B-51	
27	115.5	28.2	263	m	US-08-834-306-51	51

63 4 US-08-993-674A-51 63 4 US-08-256-976-51 00 2 US-08-167-641C-62 00 4 US-08-460-971A-62 00 4 US-08-460-971A-62 00 4 US-08-460-971A-62 00 4 US-08-460-971A-62 14 US-08-993-008-54 19 2 US-08-55-1308-54 19 2 US-08-55-1308-54 19 2 US-08-55-1308-54 19 2 US-08-55-1308-54 10 2 US-08-56-176-52 10 2 US-08-56-976-52 10 2 US-08-934-56-976-52 10 2 US-08-934-529-2 10 2 US-08-934-529-2 10 2 US-08-934-529-2 10 2 US-08-934-529-2 10 2 US-08-934-529-3 10 2 US-08-91-91-91-91-91-91-91-91-91-91-91-91-91-	Sequence 51, Appl Sequence 62, Appl Sequence 62, Appl Sequence 62, Appl Sequence 62, Appl Sequence 3, Appl Sequence 3, Appl Sequence 54, Appl Sequence 54, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 62, Appl Sequence 62, Appl Sequence 63, Appl Sequence 64, Appli Sequence 4, Appli Sequence 4, Appli
666 666 666 666 666 666 666 666	US-08-993-674A-51 US-09-256-976-51 US-08-167-641C-62 US-08-167-641C-62 US-08-460-91A-62 US-08-460-91A-62 US-08-97-830B-3 US-08-993-008A-5 US-08-93-7430B-54 US-08-93-74A-52 US-08-93-74A-52 US-09-256-976-52 US-09-344-529-2 US-09-344-529-2 US-09-344-529-2 US-09-344-529-2 US-08-312-949-4 US-08-312-949-4 US-08-312-949-4 US-08-312-949-4 US-08-312-949-4
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## ALIGNMENTS

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1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                                                                                                                              Sequence 64, Application US/08460971A

Sequence 64, Application US/08460971A

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: 613 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-460-971A-64
                                   Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.1%; Score 156; DB 4; Length 100;
                                 38.1%; Score 156; DB 3; Length 10
55.3%; Pred. No. 3.7e-08;
tive 6; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTEXT 0.5...

ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" DISKETTE, 1005 5.0
SOFTWARE: FRASES OF WINDOWS 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,971A
FILING DATE: June 5, 1995
CLASSIFICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
APPLICATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
RELEFFAR: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARATTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                       62 AKAKAKAKAKAKAKAKAKA 86
                                                                                                                                                                                   59 AKYKAEAAKKAYKAEAAKAAAKEAA
                                 Query Match
Best Local Similarity 55.33
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
 US-08-167-641C-64
                                                                                                                                                                                                                                                                                         US-08-460-971A-64
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                                                                                                                                                                Gaps
                                                                                                                                                                                                   1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                                                                                                                                                                                                                      "Lys Ala" in positions 3 to 100 may be present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.
                                                                                                                         Query Match
38.1%; Score 156; DB 2; Length 100;
Best Local Similarity 55.3%; Pred. No. 3.7e-08;
Matches 47; Conservative 6; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                               62 AKAKAKAKAKAKAKAKAKAK 86
                                                                                                                                                                                                                                                                        59 AKYKAEAAKKAYKAEAAKAAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                    OTHER INFORMATION:
; OTHER INFORMATION:
US-08-460-890A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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us-09-816-989a-6.open.rai

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18-09-041-889-27
Sequence 27, Application US/09041889
SEQUENCE OF INVENTION: Userative Colitis, and Clinical Subtypes Thereof, Using TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 35.9%; Score 147; DB 3; Length 214; Best Local Similarity 50.0%; Pred. No. 5.5e-07; Matches 47; Conservative 3; Mismatches 34; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AKKVAK--KAPAKKATKAAKKAATKAPARKAATKAPAKKAATKAPAKKAVKATKSPAKKV 168
   1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
                                          1 AKKYAKKEKAYAKKAEKAAKKAEAK-----AYKAAEAKKKAKAEAKKYAKAAKAEKKEY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 AAAEAK--YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           62 AKAKAKAKAKAKAKAKAKAKA 86
                                                                                                                                           59 AKYKAEAAKKAYKAEAAKAAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-216-894-10; Application US/08216894; Sequence 10, Application US/08216894; Patent No. 5876734; GENERAL INFORMATION: APPLICANT: Kirchhoff, Louis V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-09-041-889-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
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                                          Gaps
                                                                                                       1 AKKYAK-KEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAE 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.1%; Score 156; DB 4; Length 100; Best Local Similarity 55.3%; Pred. No. 3.7e-08; Matches 47; Conservative 6; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 64.7554

Sequence 61.7554

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
1 Similarity 55.3%; Pred. No. 3.7e-08; 47; Conservative 6; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTITY 0.5.4.

ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: BIS GONDATIBLE
COMPUTER: BIS COMPACE: DOS 5.0
SOFTWARR: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: Unue 5, 1995
CLASSIFTCATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
ANDER CONTROL PROGRAFIED CONTROL PORTROL PORTRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212/078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                            59 AKYKAEAAKKAYKAEAAKAAAKEAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 212/0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEX: (273) 955-0440
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   62 AKAKAKAKAKAKAKAKAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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STRANDEDNESS: sir
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-462-040-64
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5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPEDUBENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.6%; Score 137.5; DB 4; Length 48.9%; Pred. No. 9.5e-06; tive 11; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE PATENTIN STILL STATEMY SOFTWARE BY SOFTWARE PATENTIN BATA:
APPLICATION UNMER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BERY. Stephen A.
REGISTRATION NUMBER: 95,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELEPONMUNICATION INFORMATION:
TELEPAX: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.6%; Score 137.5; DB 2;
48.9%; Pred. No. 1.1e-05;
tive 11; Mismatches 29;
                                                                                                                                                                 85326/102/DRLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403 TKVAEAEKQKAAEATKVAEAEKQKAAEA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 KYKAEAAK-KAYKAEAAKAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION UNDRER: 29,768
REFERENCE/DOCKET NUMBER: 8532/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08216894
Patent No. 5876734
                                                                                                                                                                                                                                                                                         TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          564 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.64
Query Match
Best Local Similarity 48.94
Matches 43; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-115-746-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 43, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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US-09-115-746-10

i Sequence 10, Application US/09115746

i Patent No. 6228601

i GENERAL INFORMATION:

APPLICANT: Kirchhoff, Louis V.

APPLICANT: Kirchhoff, Louis V.

APPLICANT: Kirchhoff, Louis V.

TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION

TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLGY & Lardher

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007-5109

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC Compatible

COMPUTER: IBM FC Compatible

COMPUTER: IBM FC COMPATER

COMPUTER

COMPUTER

COMPATER

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                        APPLICANT: Otsu, Keiko
TITLB OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEBS: Folley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
33.6%; Score 137.5; DB 2; Length 4
Best Local Similarity 48.9%; Pred. No. 9.5e-06;
Matches 43; Conservative 11; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PETENT FC-D03/N3-D03
SOFTWARE: PETENT RELEASE #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMONICATION: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        403 TKVAEAEKQKAAEATKVAEAEKQKAAEA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 KYKAEAAK-KAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-216-894-10
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAAAEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 643;
  POLYPEPTIDES FOR DIAGNOSING INFECTION WITH TRYPANOSOMA CRUZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYPEPTIDES FOR DIAGNOSING INFECTION WITH TRYPANOSOMA CRUZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT IMFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INVERE: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEFRAME (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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33.6%; Score 137.5; DB 2
Best Local Similarity 48.9%; Pred. No. 1.3e-05;
Matches 43; Conservative 11; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Octsu, Kelko
ITITLE OF INVENTION: POLYPEPTIDES FOR DIAGNC
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES:
OCRRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Larder
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1 . . .
TITLE OF INVENTION: POLYPEPTIDES FOR DIAC TITLE OF INVENTION: WITH TRYPANOSOWA CRUZ NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519 TKVAEAEKOKAAEATKVAEAEKOKAAEA 546
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                                                                                                                                                                        ZIP: 20007-5109
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDIUM TYPE: Floppy disk
CMEDIUM TYPE: Floppy disk
CMEDIUM TYPE: Floppy disk
CMEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: 08/216,894
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-115-746-8
; Sequence 8, Application US/09115746
; Patent No. 6228601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         643 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-216-894-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                            usa
                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                           1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAK-AEKKEYAAAEA 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.6%; Score 137.5; DB 4; Length 564; Best Local Similarity 48.9%; Pred. No. 1.1e-05; Matches 43; Conservative 11; Mismatches 29; Indels 5.
                                                                                                                                                                                                                                    US-09-115-746-2

Sequence 2, Application US/09115746

Patent No. 6228601

GENERAL INFORMATION:

APPLICANT: Kitchhoff, Louis V.

APPLICANT: Otsu, Keiko

TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: WEAL COUNTRY: USA
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILING DATE:
PRIOR APPLICATION NUMBER: 08/216,894
FILING DATE:
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                          ||| | || :| | || 491 TKVAEAEKQKAAEA 518
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                                                                                                          60 KYKAEAAK-KAYKAEAAKAAAKEAAYEA 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFRENCE/DOCKET NUMBER: 8532
TELECOMMUNICATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-216-894-8
; Sequence 8, Application US/08216894
; Patent No. 5876734
; GENERAL INFORMATION:
; APPLICANT: Kirchhoff, Louis V.
; APPLICANT: Otsu, Keiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELERAS: (202)672-5399
TELER: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: protection
US-09-115-746-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202) 672-5300
(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1(CORRESPONDENCE ADDRESS: ADDRESSEB: Foley & La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
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MOLECULE TYPE: protein
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         ; MULECULE ;
US-08-346-849-2
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Fatent No. 5670483
GENERAL INFORMATION:
APPLICANT: Lockshin, Curtis
APPLICANT: Lockshin, Curtis
APPLICANT: Lockshin, Curtis
APPLICANT: Lockshin, Curtis
APPLICANT: Holmes, Todd
ITILE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS: 64
CORRESPONDENCE ADDRESS:
ADDRESSER: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 ATKVAEAEK---QKAAEATKVAEAEKQXAAEATKVAEAEKQKAAEATKVAEAEKQXAAEA 518
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.6%; Score 137.5; DB 4; Length 643; Best Local Similarity 48.9%; Pred. No. 1.3e-05; Matches 43; Conservative 11; Mismatches 29; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTER TRADABLE FORM:

ZIP: 02173-479
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
                          REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
TELERA: 90413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, DAVIG E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: 24,592
REFERENCE/DOCKET NUMBER: MIT-6008
TELECHONE: (617) 861-6240
TELECHONE: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               519 TKVAEAEKOKAAEATKVAEAEKOKAAEA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 KYKAEAAK-KAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                         INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 643 amino acids TYPE: amino acids TOPOLOGY: linear
  ATTORNEY/AGENT INFORMATION:
                        NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-09-115-746-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-08-346-849-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKYAKKEKAYAKKAEKAAKKAEAAKAYKAAEAKKKAKAEAKKYAKA-AKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Edung, Shuguang
APPLICANT: Zhang, Shuguang
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, ABexander
APPLICANT: Diebersio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORNED BY
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: TWO MILITIA Drive
Query Match 32.6%; Score 133.5; DB 1; Length 433; Best Local Similarity 47.6%; Pred. No. 2e-05; Matches 40; Conservative 12; Mismatches 25; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 433;
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SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/293,284A

FILING DATE: 22-AUG-1994

CLASSIFICATION: 435

RIOR APPLICATION DATA:

APPLICATION NUMBER: 07/973,326

FILING DATE: 28-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: BROOK, DAVIG E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: 22,592

REFERENCE/DOCKET NUMBER: MIT-6008A

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.6%; Score 133.5; DB 2; 47.6%; Pred. No. 2e-05; tive 12; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Lexington
STATE: Masachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                           US-08-293-284A-2; Sequence 2, Application US/08293284A; Patent No. 5955343
                                                                                                                                                                                                                                     61 YKAEAAKKAYKAEAAKAAAKEAAY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YKAEAAKKAYKAEAAKAAAKEAAY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 433 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 40; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Search completed: March 10, 2003, 12:30:03 Job time : 15.2405 secs
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                                                                                         1 AKKYAKK---EKAYAKKAEKAAKKAEAK--AYKAAEAKKKAKAEAKKYAKAAKAEKKEYA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.7%; Score 129.5; DB 4; Length 223; Best Local Similarity 54.3%; Pred. No. 2.4e-05; Matches 50; Conservative 5; Mismatches 26; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,347
FILING DATE: 29-40G-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 AAPAK-KAPAKKAATKAAPAKKAPAKKAATKA 198
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345 EAAKAAKKKNK-RAIRNSAKEADY 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INPORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                   RESULT 14
US-09-095-855-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-095-855-201
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RESULT 15 82.09-205-426-201 ; Sequence 201, Application US/09205426 ; Patent No. 6406704

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Indels 11; Gaps
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GRENKALL INFORMATION:
GRENKALL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Fan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: DIAGNOSIS of Mycobacterial Infections FILE REFERENCE: 11000.10024
CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 09/995,855
FRALIER APPLICATION NUMBER: 08/997,362
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER PILING DATE: 1999-06-12
EARLIER PILING DATE: 1999-06-12
EARLIER PILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
EBRCIAL 23

LENGHAL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 31.7%; Score 129.5; DB 4; Length 223; Best Local Similarity 54.3%; Pred. No. 2.4e-05; Matches 50; Conservative 5; Mismatches 26; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 AAPAK-KAPAKKAATKAAPAKKAPAKKAATKA 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mycobacterium vaccae US-09-205-426-201
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9

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5.1.3
Compugen Ltd.
version 9
GenCore (c) 1993 .
       Copyright
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OM protein - protein search, using sw model

March 10, 2003, 12:15:04 ; Search time 31.9641 Seconds
 (without alignments)
327.825 Million cell updates/sec Run on:

US-09-816-989A-7 519 Title: Perfect score:

1 AKKYAKKAEKAYAKKAKAK.......AKAYKAEAAKAAAKEAAYEA 109 Sequence:

Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* 4 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	tolA protein - Esc	membrane spanning	membrane spanning	ne H	TolA protein PA097		icin	mst101-1 protein -	histone H1-beta, e	sperm tail-specifi	histone H1, gonada	Ľ,		histone H1 - Chlam	cgcr-4 protein - C	hypothetical prote	outer membrane pro	U	histone H1.11L - C	R27-2 protein - Tr	tolA protein VC183	cytosolic repetiti	₽.	•	histone H1-5 [vali	H1.11	4	mon - ch	histone H1.01 - ch
SUMMARIES	ΩI	JV0057	F90725	G85576	A25550	E83525	AG0592	AC0138	S34153	A28100	S51364	HSUR1P	T09127	A28456	859589	\$19113	T17698	B43592	S61926	B28456	T30296	A82152	A44993	E60110	HSTRIR	S51660	C28456	HSHU1B	A33430	A23055
	DB	7	~	0	~	7	ณ	N	~	7	7	Н	~	N	~	N	7	~	~	~	~	N	۲	~	Н	Н	0	٦	Н	7
	Query Match Length	421	394	394	210	347	376	388	344	211	1390	248	1701	220	231	265	311	384	182	225	1128	356	328	219	206	226	219	219	771	218
de	Query		35.0	35.0	34.9	4.	34.3	4	•	33.2	33.0	ς.	ď		ä	31.6	ä	31.5	31.4	ä		•	ä	ä	30.9	ö	ö	°.	30.3	30.2
	Score	189.5	181.5	181.5	181	179	178	178	175.5	172.5	171.5	170.5	170.5	165	164.5	164	164	163.5	163	163	162.5	162	161.5	161	160.5	9	159.5	158	-	156.5
	Result No.	-	~	٣	4	ഗ	9	7	80	σ	10	11.	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

178 AAAEAQKKAEAAAAALKKKAEAAEAAABAEAKKKAATEAAEKAKAEAEKKAAAEKA 232

RESULT 2 F90725

g

hypothetical prote histone H1-II - Vo	polyhydroxyalkanoa	conserved nypotnet outer membrane int	histone H1.03 - ch	probable translati	histone H1 - mouse	histone H1-gamma,	histone H1 (clone	histone H1 - musco	histone H1 - mouse	histone H1.1 - Cae	histone H1 - mouse	hypothetical prote	regulatory protein
S29309 JN0748	G83013	H71321 G64064	D28456	T11583	A28470	A26721	T06257	S01262	149742	T23778	S49482	AE1689	A35630
~ ~	~	N (7	7	~	N	N	N	7	N	7	~	0	7
217	309	372	224	1403	212	217	288	218	219	208	221	243	340
29.8	29.8	29.6	29.4	29.1	28.9	28.9	28.9	28.5	28.4	28.3	28.3	28.3	28.3
154.5 29.8 154.5 29.8								148 28.5					

#### ALIGNMENTS

RESULT 1

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tolA protein - Bscherichia coli (strain K-12)
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002
C;Accession: JV0057; B64810
R;Levengood, S.K.; Webster, R.B.
J. Bacteriol. 171, 6600-6609, 1989
A;Title: Nuclectide sequences of the tolA and tolB genes and localization of their produces of the collaboration of the collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-421 cLEV>
A; Residue: 1 clev: 1 cle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-421 < BLAA
A;Residues: 1-421 < BLABO0177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960;
A;Experimental source: strain K-12, substrain MG1655
C;Comment: tolA and tolB proteins are necessary for collcins E2, E3, A, and K to reach t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
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Best Local S
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A; Reference number: A25550; MUID: 87040778; PMID: 3022245
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A;Molecule type: DNA
A;Residues: 1-376 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Gene: tolA; PA0971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: AG0592
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histone H1 - sea urchin (Lytechinus pictus)
Cispecies: Lytechinus pictus (painted urchin)
Cispecies: Lytechinus pictus (painted urchin)
Cipate: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
CiAccession: A25550
CiAccession: A25550
CiAccession: A25550
Nucleic Acids Res. 14, 8121-8133, 1986
Nucleic Acids Res. 14, 8121-8133, 1986
A;Title: Comparison of the late H1 histone genes of the sea urchins Lytechinus pictus an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gend
            substrain
                                                                                            Ω
Ω
membrane spanning protein TolA [imported] - Escherichia coli (strain 0157:H7, substri C;Species: Escherichia coli C;Decies: Escherichia coli C;Decies: Escherichia coli C;Decies: Bull-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, (gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: F90725 A;Actus: preliminary A;Actus: preliminary A;Residues: 1-394 cHAY> A;Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GN00154 A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKAE----KAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAK-EAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKAE----KAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAK-EAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAEAQKKABAAAALKKKABEAABAABARKKAAABKAAADKKAABKAAABKAA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 AKKBAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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                                                                                                                                                                                                                                                                                                                                                                                     35.0%; Score 181.5; DB 2; Length 394; 52.2%; Pred. No. 4.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.0%; Score 181.5; DB 2; Length 394; 52.2%; Pred. No. 4.7e-05; tive 12; Mismatches 32; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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60; Conserv
                                                                                                                                                                                                                                                                                                                                            A; Gene: EC80774
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83525
C;Accession: E83525
R;Stover, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradhan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 559-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <STO>
A;Ecssreferences: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001
C;Genetics:
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; PMID:11677608
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                                                                                                                                                                                                                                                                                                                       4,
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A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                           99 OKLEGOGVAAAKAAEGKKADEARKAEAGKAAEAKKADEAKKAAEAKAAEGKKGADIAKKR 158
                                                                                                                                                                                                                                                                                                                                                                                   2 KKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAE----AKKKAKAEAKKYAKEAAKAK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 KKAEKAYAKKAKAKAKEK-----KAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 KEAYKAEAKKYAKAAKAEKKEYAAAEAKKA-----EAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A25550
A;Molecule type: DNA
A;Residues: 1-210 «CNOX)
A;Cross-references: GB:X04488; NID:g9616; PIDN:CAA28177.1; PID:g9617
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
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                                                                                                                                                                                                                                                                                                               36; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                           Query Match

34.9%; Score 181; DB 2;
Best Local Similarity 50.0%; Pred. No. 3.2e-05;
Matches 58; Conservative 8; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.5%; Score 179; DB 2;
49.1%; Pred. No. 6.1e-05;
tive 17; Mismatches 29;
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Best Local Similarity 49.19
Matches 54; Conservative
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C;Accession: A28100
R;Lai, Z.C.; Childs, G.
Nol. Cell. Biol. 8, 1842-1844, 1988
A;Title: Characterization of the structure and transcriptional patterns of the gene encoma, Reference number: A28100; MUID:88246461; PMID:2837660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Drosophila hyde:
C;Species: Drosophila hyde:
C;Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 23-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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A;Acoss-references: GB:M20314
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; embryo; nucleosome; nucleus
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                                                                                                                                                  1 AKKYAKKAEK----AYAKKAKAAKEKKAYAKKEAKAYKAAE-----AKKKAKAKAEAKKY 49
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                                                                                                                                                                                                                                                                                      50 AKEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKK-AEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                           sea urchin (Strongylocentrotus purpuratus)
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A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
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       Length 344;
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Score 175.5; DB 2;
Pred. No. 0.0001;
8; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 172.5; DB 2,
Pred. No. 0.00011;
9; Mismatches 40;
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A,Status: nucleic acid sequence not shown
A,Roblecule type: DNA
A,Residues: 1-1390 «NEE>
A,Cross-references: EMBL:X73481
A,Rossen, J.; Heinlein, U.A.O.; Buenemann, H. submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: FlyBase: FBgn0011816
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   33.8%;
Similarity 49.2%;
68; Conservative 8
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Rest Local Similarity 48...
5; Conservative
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   Query Match
Best Local Simi
Matches 58;
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CiDate: OZ.Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
CiDate: OZ.Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
CiACCession: AC0138
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Status: preliminary
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   A;Cross-references: GB:AL513382; PIDN:CAD05209.1; PID:g16501979; GSPDB:GN00176
C;Genetics:
A;Gene: STY0793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-388 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89966.1; PID:g15979190; GSPDB:GN00175
C;Genetics:
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34153
R;Nessen, J.; Heinlein, U.A.O.; Buenemann, H.
Bubmitted to the EMBL bata Library, June 1993
                                                                                                                                                                                                                                                                                                                              54 AKAKKEAYKAEAKKYAKAAK-----AEKKEYAAAEAKKAEAAK--AYKAEAAKAAAKEA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 AAAKKQA-DADAKKAVEVAEKAAADAAEKKAAADAE-KKAAAAKKVAAAAEAKKKAAAEA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 KQAAEQQKIAAAAVAKAKEEQKQAETAAAQAKAEADKIVKAQAEAQKKAEAEAKKEAAVA 199
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                  1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAAEAKKKAKAEAKKYAKEAAKAKKEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKYAKKAEKAYAKKAKAKAKEKK-----AYAKKEA-KAYKA-AEAKKKAKAEAKKYAKEA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAA---KEAAYE 108
                                                                                                                                                  Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 388;
                                                                                                                                           Query Match 34.3%; Score 178; DB 2; Length 376 Best Local Similarity 52.3%; Pred. No. 7.5e-05; Matches 58; Conservative 10; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: EMBL:X73480, NID:g313199, PID:g313200
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mst101-1 protein - fruit fly (Drosophila hydei)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: FlyBase:Dhyd/mst101
A;Cross-references: FlyBase:FBgn0011816
C;Superfamily: neurofilament triplet H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Accession: S34153
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-344 <NEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 A 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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C;Dapecies: Chlamydomonas reinhardtii
C;Date: 10-Apr-1996 Heaquence_revision 19-Apr-1996 #text_change 23-Jul-1999
C;Accession: S59589; S62122
R;Fabry, S.; Mueller, K.; Lindauer, A.; Park, P.B.; Cornelius, T.; Schmitt, R.
Curr. Gener. 28, 333-345, 1995
A;Title: The organization structure and regulatory elements of Chlamydomonas histone general R;Reference number: S59581; MUID:96120862; PMID:8590479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Status: nucleic acid sequence not shown
A, Status: nucleic acid sequence not shown
A, Residues: 1-231 <FAB>
A, Molecule type: DNA
A, Residues: 1-231 <FAB>
A, Cross references: EMBL: U16726
A, Note: references: EMBL: U16726
B, Risabry, S.; Ford, C.; Lindauer, A.; Mueller, K.; Cornellus, T.; Schmitt, R.
submitted to the EMBL Data Library, October 1994
A, Bescription: The organization, structure and controlling elements of Chlamydomonas histly A, Reference number: S62122
A, Rocession: S6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: histone H1
C;Keywords: acetylated amino end; chromosomal protein; DNA binding; nucleosome; nucleus
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 histone H1.10 - chicken
C;Species: Gallus gallus (chicken)
C;Daces 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 04-Mar-2000
C;Accession: A24456
R;Coles, L.S.; Robins, A.J.; Madley, L.K.; Wells, J.R.E.
J. Biol. Chem. 26., 9565-963, 1987
A;Fitle: Characterization of the chicken histone H1 gene complement. Generat
A;Reference number: A92655; MUID:87250632; PMID:3597432
                                                109 SKKPGEVKEKAPRKRTPAAKPRAAKKPASAAKKPKAAAAKKSPKKAKKPAAATKKA 168
    63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Accession: A28456
A, Molecule type: DNA
A, Residues: 1-220 <COL>
A, Cross-references: GB:M17018, NID:g211834; PIDN:AAA48788.1; PID:g211835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEA----KAYKAAEAK---KKAKAEAKKYAKEA
    5 АККАБКАУАККАКАККАУАККЕАКАУКААБАКККАКАБАККУАКЕААКАККЕАУКА-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 AKAKKEAYKAEAKKYAKAAKAEKKEYAA-AEAKKAEAAKAYKAEAAKAAAKE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 31.8%; Score 165; DB 2; Length 220; Best Local Similarity 46.4%; Pred. No. 0.00034; Matches 52; Conservative 11; Mismatches 41; Indels
                                                                                                                                                                                                                        A;Introns: 62/3; 101/3
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome
                                                                                                                                                                       64 EAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     histone H1 - Chlamydomonas reinhardtii
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Best Local Similarity 45.94
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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                                                                                                                                                                                                                                                                                                                                                            HSULT 11
HSURIP
C.SPecies: Parechinus angulosus (angulate urchin)
C.Species: Parechinus angulosus (angulate urchin)
C.Species: Parechinus angulosus (angulate urchin)
C.Species: 31-Mar-1980 #sequence_revision 31-Mar-1980 #text_change 16-Feb-1997
C.Accession: A91090; A01091; A05866
R.Strickland, W.N.; Strickland, M.; de Groot, P.C.; von Holt, C.; Wittmann-Liebold, B.
Eur. J. Biochem: 104, 559-566, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus ang A;Contents: sequence of residues 1-84
A;Accession: A91090
A;Molecule type: protein
A;Residues: 1-248 <STR>
R;Strickland, W.N.; Strickland, M.; Brandt, W.F.; von Holt, C.; Lehmann, A.; Wittmann-Liebur, J. Biochem: 104, 567-578, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus ang A;Residues: 80-248 <ST2>
A;Molecule type: protein
A;Residues: 80-248 <ST2>
A;Molecule type: protein
A;Residues: 80-248 <ST2>
A;Molecule type: protein
A;Residues: 80-248 <ST2>
A;Note: 144-Arg was also found
C;Superfamily: histone H1
C;Keywords: DNA binding; nucleosome; sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable erythrocyte-binding protein MAEBL - Plasmodium yoelii

C;Species: Plasmodium yoelii

C;Species: Plasmodium yoelii

C;Accession: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C;Accession: T09127

R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.

R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.

R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.

R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.

A;Reference number: 216577; MUD:98115903; PMID:9448314

A;Reference number: 216577; MUD:98115903; PMID:9448314

A;Retous: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-1701 KARP>

A;Residues: 1-1701 KARP>

A;Residues: 1-1701 KARP>

A;Cross-references: EMBL:AF031886; NID:92947227; PID:92947228
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                                                    120 KKAKKTSAAAKKKAKAKAAAKKAKAKAAAKKKAALAKKKAAAAKRKAAAKAKKKKK 179
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                                                                                                                                                                                                                        50 AKEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
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A;Introns: 62/1; 1648/1; 1674/2; 1697/1
C;Keywords: alternative splicing; cell binding; erythrocyte invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 248;
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1 AKKYAKKAEKAY----AKKAKAKAKEKKAYAKKEAKAYKAAE-
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2 KKYAKKA---BKAYAKKAKAAKEKKAYAKKEA----KAYKAAEAKKKAKAEAKKYAKEAA 54

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RESULT 15
S19113
cgcr-4 protein - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: S19113; S1446
R;WakAsrchuk, ww. w., Wu., Puller, F.W.; Beck, C.F.
Plant Mol. Biol. 18, 143-146, 1992
A;Title: Two GC-rich DNA elements of Chlamydomonas reinhardtii with complex arrangements
A;Reference number: S19113; MUD:92119224; PMID:1731966
A;Accession: S19113
A;Status: prediminary
A;Molecule type: DNA
A;Residues: 1-265 <WAK>
A;Cross-references: EMBL:X17208; NID:g18136; PIDN:CAA35080.1; PID:g18137
C;Genetics:
A;Genetics:
A;Genetics:
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55 KAKKEAYKAEAKKYAKAA----KAEKKEYAAAE---AKKAEAAK---AYKAEAAKAAAKE 104
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31.6%; Score 164; DB 2; Length 265;
Best Local Similarity 39.4%; Pred. No. 0.00045;
Matches 50; Conservative 21; Mismatches 38; Indels 18;
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SA 221
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79 AEAKAKEADEARADEBRANABANABABEARABABANAABEANAAABABANAABABAAAAA 138
47 KKYAKEAAKKEAYKKEAYKAEAKKYAKAAK ---BEKKEYAABAKKABAAKYKABAAKAA 102
139 RVAAERAAAAAABAAAAKAKAVAAEAAAAAABAAAAAAAAA 198

Search completed: March 10, 2003, 12:28:30 Job time : 32.9641 secs

103 KEAAYEA 109 : | | | 199 EAKAKEA 205

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OM protein - protein search, using sw model

March 10, 2003, 12:15:01 ; Search time 24.8354 Seconds
 (without alignments)
 182.035 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-816-989A-7 519 1 AKKYAKKABKAYAKKAKAAK......AKAYKABAAKBAAYBA 109

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_40:\* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		Description	34		P50600 pseudomonas						trepone		oncor	P16401 homo sapien	Q9zhc5 mycobacteri	P08288 gallus gall	P10412 homo sapien	P12957 gallus gall	gallus	Q08865 volvox cart			Q10475 schizosacch		-		P09426 anas platyr	TUB T	caen		P09987 gallus gall	37			
SUMMARIES		OI.	TOLA ECOLI	H1_LYTPI	TOLA PSEAE	MST1_DROHY	MST2_DROHY		H1B_STRPU	H110_CHICK	TMPB_TREPH	H11L_CHICK	H1_ONCMY	H15_HUMAN	DBH_MYCSM	H11R_CHICK	H14_HUMAN	CALD_CHICK	H101_CHICK	H12_VOLCA	TOLA_HAEIN	H103_CHICK	YDF3_SCHPO		HIG_STRPU	ASR_KLEPN	H1_ANAPL	H14 MOUSE	H11_CAEEL	H13_MOUSE	H1 CHICK	RLZ2_DROME			H12_RAT
		Match Length DB	421 1	210 1	347 1	344 1	1391 1	248 1	211 1	219 1	384 1	224 1	206 1	225 1	208 1	218 1	218 1	771 1	218 1	240 1	372 1	223 1	1403 1	211 1	217 1	139 1	217 1	218 1	207 1	220 1	217 1	299 1	232 1	352 1	218 1
	* Query	Match	36.5	•	34.5	ω.		32.9	32.7	31.8	31.5	31.4	30.9	30.9	30.8	30.7	30.4	30.3	٠.	29.8	29.6	29.4	29.1	28.9	28.9	ω.	28.5	28.4	28.3	28.3	28.1	28.1	27.7	27.7	27.6
		Score	189.5	181	179	175.5	171.5	170.5	169.5	165	163.5	163	160.5	160.5	160	159.5	158		156.5	154.5	S	152.5	151	150	150	148		147.5	147	147	146	146	144		143.5
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09 mycobacteri 77 chironomus 54 salmo trutt 76 chironomus 51 aedes aegyp 75 chironomus 51 oryctolagus 53 homo saplen 64 volvox cart 64 volvox cart 64 homo saplen 65 chironomus 78 chironomus 78 chironomus
P95109 P40277 P40276 P40276 P40276 P40275 P60275 P60275 P60278
DBH MYCTU HIC_CHITE HIB_CHITE RS6_AEDAE HIA_CHITE HI3_RABIT BASF_HUMAN HI1_VOLCA NFH HUMAN HIE_CHIPE HIE_CHIPE
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# ALIGNMENTS

us-09-816-989a-7.open.rsp

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MEDLINE=87040778; PubMed=3022245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X04488; CAA28177.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A25550; A25550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tola protein.
TOLA OR PA0971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=PAO;
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P50600;
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à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Late histone H1.
Lytechinus pictus (Painted sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euchinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKAE----KAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAK-EAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: INTERACTS, VIA DOMAIN II, WITH PORINS OMPC, PHOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transport; Protein transport; Bacteriocin transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                             MEDLINE=99332679; PubMed=10404600; Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.; Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.; Filamentous phage infection: crystal structure of g3p in complex with its coreceptor, the C-terminal domain of TolA."; Structure 7:711-722(1999).

-I-FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP A COLICINS (COLICINS A, B1, B2, B3, AND K). NECESSARY FOR THE COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL BINDING TO THE BACTERIA. ALSO INVOLVED IN THE TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PERIPLASNIC (POTENTIAL).
DOMAIN II (ALPHA-HELICAL).
DOMAIN III (FUNCTIONAL).
10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 AAAEAQKKAEAAAALKKKAEAAEAAAEARKKAATEAAEKAKAEAEKKAAAEKA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
              "TolA central domain interacts with Escherichia coli porins.";
EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.5%; Score 189.5; DB 1; Length 421; 53.0%; Pred. No. 6.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; Inner membrane; 3D-structure; Complete proteome. DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
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                                                                                                         X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421.
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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EMBL; AE000177; AAC73833.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 AA; 43156 MW;
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                                                                                                                                                                                                                                                                                                                                                                                         OF BACTERIOPHAGE DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Conservative
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PDB; 1TOL; 20-MAY-99.
EcoGene; EG11007; tolA.
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421
310
421
278
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Lloubes R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lytechinus.
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P06144;
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H. LYTPT
L. H. LYTPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, MASSSY, LAST.
HSSP, MASSY, LAST.
HSSP, PO2259, 1HST.
INTEXPRO; IPR001386; Histone H1/H5.
INTEXPRO; IPR001326; Linkerhist N.
Probom; PD000339, linkerhist N; I.
Probom; PN00526; H15; 1.
SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE=20431337; PubMed=10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 KEAYKAEAKKYAKAAKAEKKEYAAAEAKKA-----EAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 КРАККААККРААК--КААККРААККРАККААККРАККААКРАККААККРАККАА 208
Knowles J.A., Childs G.J.;
"Comparison of the late H1 histone genes of the sea urchins
Lytechinus pictus and Strongelocentrotus purpuratus.";
Nucleic Acids Res. 14:8121-813 (1986).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SUBCELLULAR LOCATION: Nuclear.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dennis J.J., Lafontaine E.R., Sokol P.A.; "Identification and characterization of the tolQRA genes of Pseudomonas aeruginosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duan K., Sokol P.A.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.9%; Score 181; DB 1;
50.0%; Pred. No. 1.3e-05;
iive 8; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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"The Drosophila hydei gene Dhmatlol(1) encodes a testis-specific,
"The brosophila hydei gene Dhmatlol(1) encodes a testis-specific,
Tepetitive, axoneme-associated protein with differential abundance in
Y chromosomal deletion mutant flies.";
Dev. Biol. 162:414-425(1994).
-i- FUNCTION: POSSIBLE STRUCTURE ROLE IN THE SPERM TAIL. IT IS
ASSOCIATED WITH AXONEMAL STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OKLEQQQVAAAKAAEQKKADEARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 KKAEKAYAKKAKAAKEK-----KAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKE 59
                                                                                                                                                                                                                                                                                                                                                                                                                         Transport, Protein transport, Transmembrane, Repeat, Inner membrane,
Complete proteome.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                          SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                  -! - FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPERMATID BUNDLES.
DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN STRAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic (By similarity). TISSUE SPECIFICITY: TESTIS. LOCATED IN SPERMATOCYTES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 AYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKABAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 347 PERIPLASMIC (POTENTIAL).
209 216 POLY-ALA.
347 AA; 37935 MW; EEDD4B04AAQ95945 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
PERIPLASMIC (POTENTIAL).
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 179; DB 1;
Pred. No. 2.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Axoneme-associated protein mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94200512; PubMed=8150205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.5%;
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U39558; AAC44660.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MST101(1).
Drosophila hydei (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE004530; AAG04360.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                  opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
37
347
216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                          (BY SIMILARITY
                                                                                                                                                                                                (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muscomorpha; Eph
NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MST1 DROHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MST101(1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
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-!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
-!- POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWREN DIFFERENT
-!- STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 X 16 AA APPROXIMATE TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKAEK----AYAKKAKAKAKAKAYAKKEAKAYKAAE-----AKKKAKAEAKKY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 AKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAERKK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila hydei (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 AKEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKK-AEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mesen J., Padmanabhan S., Buenemann H.;
"Tandemly arranged repeats of a novel highly charged 16-amino-acid
motif representing the major component of the sperm-tail-specific
axoneme-associated protein family Dhmst101 form extended
alpha-helical rods within the extremely elongated spermatozoa of
Drosophila hydei.";
Eur. J. Blochem. 225:1089-1095(1994).
-I- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL.
-I- SUBCELBULAR LOCATION: Cytoplasmic.
-I- SUBCELBULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -K-X-X-E-X-A-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K-K-C-X-E-X-A-[KQ]-K-X-344 AA; 37793 MW; 24C65D2510387E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 4.2e-05;
8; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
10-FEB-1995 (Rel. 31, Last sequence update)
10-CTT-2001 (Rel. 40, Last annotation update)
Axoneme_associated protein mst101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.8%; Score 175.5; 49.2%; Pred. No. 4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1391
                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                           FlyBase, FBgn0011816, Dhyd\mst101(1).
Sperm, Repeat, Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95045538; PubMed=7957199;
                                                                                                                                                                                                                                                                                                                 EMBL; X73480; CAA51875.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X73481; CAA51876.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 49.29
Watches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           337
                                                                                                                                                                                                                                                                                                                                                         PIR; S34153; S34153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S34154; S34154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DROHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MST101(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           Sperm; DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
000000000008888FF8
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                                        62
                                                                                                                      H1B_STRPU
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                                                                                                                                                           1068 AKKLIKEAAEKKOCEERAKKEKEAAEKKOCEERAKKLIKEAAEKKOCEERAKKEKEAAEKKR 1127
             MEDLINE-80156832; PubMed-7363905;
Strickland W.N., Strickland M., Brandt W.F., von Holt C., Lehmann A.,
Wittmann-Liebold B.;
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The primary structure of histone HI from sperm of the sea urchin Parechinus angulosus. 2. Sequence of the C-terminal CNBr peptide and the entire primary structure.";

Eur. J. Biochem. 104:567-578(1980).
-!- FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                   1 AKKYAKKAEKAY----AKKAKAAKEKKAYAKKEAKAYKAAE-----AKKKAKAEAKKY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 1. Chemical and enzymatic fragmentation of the protein and the sequence of amino acids in the four N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM06526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                1128 CBEAAKREKEA--AEKKKCAEAAKKEKE--ATEKOKCAEAAKKEKEAAEKKKCAEAA 1180
                                                                                                                                                                                       50 AKEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                                                                                                          15;
                                                                               DB 1; Length 1391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.9%; Score 170.5; DB 1; Length 248; 46.0%; Pred. No. 6.7e-05; tive 9; Mismatches 41; Indels 11.
                                                                                                                                                                                                                                                                                                                                                 Histone H1, gonadal.
Parechinus angulosus (Angulate sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida, Echinidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=80156831; PubMed=6767609;
Strickland W.N., Strickland M., de Groot P.C., von Holt C.,
Wittmann-Liebold B.;
                                                                              Query Match 33.0%; Score 171.5; DB 1; Length 1: Best Local Similarity 46.2%; Pred. No. 0.00022; Matches 54; Conservative 11; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 K -> R.
26387 MW; 1B25B3F136541947 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: SPERM.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
PIR; A02586; HSURIP.
                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                   248 AA
FlyBase; FBgn0020733; Dhyd\mst101(2)
                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyanogen bromide peptides.";
Eur. J. Biochem. 104:559-566(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; Linkerhist N.
Pfam; PF00538; linker histone; I.
ProDom; PD000373; Linkerhist N; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 46.0 Matches, 52; Conservative
                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 80-248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P02259; 1HST
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-84.
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7658;
                                                                                                                                                                                                                                                                                                           21-JUL-1986
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                          Parechinus
                                                                                                                                                                                                                                                                                   H1 PARAN
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5

Gaps

41; Indels 11;

2 KKYAKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEAY 61

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                                  120 KKAKKTSAAAKAKKAKAAAAKKAKAKAAAKRKAALAKKKAAAAKRKAAAKAKKKKK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoldea, Euechinoidea, Echinacea, Echinoida, Strongylocentrotidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-88246461; PubMed-2837660;
Lai Z.-C., Ghilds G.;
"Characterization of the structure and transcriptional patterns of the gene encoding the late histone subtype HI-beta of the sea urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KYAKKAE-KAYAKKA--KAAKEKKAYAKKEAKAYKAAEAK-KKAKAEAKKYAKEAAK--- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P02259; 1HST.
InterPro; IPR001386; Histone H1/H5.
InterPro; IPR001318; Linkerhist N.
Pfam; PF00538; linker histone; I.
ProDom; PD000373; Linkerhist N; 1.
SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
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                                                                                                                                             180 KAAKKAKKPAKKSPKKAKKPAKKSPKKKAKRSPKKAKKAAGKRKPAAKKARR 232
                                                                                                   KA--EAKKYAK------AAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          = -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strongylocentrotus purpuratus.";
Mol. Cell. Bild. 8:1842-1844 (1988).
-i- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9F214581334BBE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.7%; Score 169.5; DB 1
48.7%; Pred. No. 6.9e-05;
iive 8; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1-beta, late embryonic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
H110 CHICK
TANDARD; PRT; 219 AA.
AC P08286;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-10V-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                          211
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EMBL; M20314; AAA30052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55; Conservative
                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A28100; A28100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strongylocentrotus.
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REPEAT
REPEAT
SEQUENCE
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                                                                                                                                                                                                                                                                                             SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3,
Histone Hl.10 (Methylated DNA binding protein-2-Hl) (MDBP-2-Hl).
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEA----KAYKAAEAK---KKAKAEAKKYAKEA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                MEDLINE-87250632; PubMed-3597432;
MEDLINE-87250632; PubMed-3597432;
Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;
"Characterization of the chicken histone H1 gene complement.
Generation of a complete set of vertebrate H1 protein sequences.";
J. Biol. Chem. 262:9656-9663(1987).
                                                                                                                                                                               MEDLINE=98060905; PubMed=9396815; Schwarz S., Hess D., Jost J.B.; "The methylated DNA binding protein-2-H1 (MDBP-2-H1) consists of histome H1 subtypes which are truncated at the C-terminus."; Nucleic Acids Res. 25:5052-5056(1997).
-! FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-! SUBCELLULAR LOCATION: Nuclear.
-! SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 AKAKKEAYKAEAKKYAKAAKAEKKEYAA-AEAKKAEAAKAYKAEAAKAAAKE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 31.8%; Score 165; DB 1; Length 21
1 Similarity 46.4%; Pred. No. 0.00014;
52; Conservative 11; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACETYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treponemal membrane protein B precursor (Antigen tmpB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 GLOBULAR.
21872 MW; A944DF6C0D3048AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  384 AA
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M17018; AAA48788.1; -.
PIR; A28456; A28456.
HSSP; PO8287; 1CHC.
InterPro; IPR001136; Histone_H1/H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00538; linker histone; 1. ProDom; PD000373; Linkerhist N; 1.
                                                                                                                                                                       IDENTIFICATION OF ALA-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00526; H15; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 AA;
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Best Local Similarity
                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acetylation.
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MOD RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,
                              Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell F., Sliviensky L., Schouls L.M., van Embden J.D., Charon N.W.; "Treponema phagedenis encodes and expresses homologs of the Treponema pallidum TmpA and TmpB proteins."; Infect. Immun. 59:3685-3693(1991).

-i- FUNCTION: TMP MAY SERVE AS A PORIN OR TRANSPORT PROTEIN FOR
                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTÏAL.
TREPONEMAL MEMBRANE PROTEIN B.
17 X 5 AA TANDEM REPEATS OF K-A-A-[AKR]-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-16.
1-17.
6 x 8 AA TANDEM REPEATS OF [EA]-A-A-R-X-
A-A-E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 KAAEEAAARKAABEAARKAAEEEAARIAAEEEAARKAAEEEAARKAAEEAIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6E94CBC74294DE8C CRC64;
                                                                                                                                          LARGE MOLECULES.
--- SUBCELLULAR LOCATION: OUTER MEMBRANE-ASSOCIATED.
--- SIMILARITY: TO TMPB OF T.PALLIDUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 163.5; DB 1
; Pred. No. 0.00026;
12; Mismatches 42
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Antigen; Outer membrane; Repeat; Signal.
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1-12.
1-14.
1-15.
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STRAIN-Kazan 5;
MEDLINE-91372983; PubMed=1894368;
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                                                                                                                                                                                                                                                                                                                                                                        EMBL; M58563; AAA27480.1; -.
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tes 52; Conserv
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ID HILL CHICK
AC P08287;
DT 01-AUG-1988
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MEDLINE=90130391; PubMed=2613692;
Ohe Y., Hayashi H., Iwai K.;
"Human spleen histone Hl. Isolation and amino acid sequences of three minor variants, Hla, Hlc, and Hld.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                     Mezquita J., Connor W., Winkfein R.J., Dixon G.H.;
"An H1 histone gene from rainbow trout (Salmo gairdnerii).";
J. Mol. Bvol. 21:209-219(1985).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.9%; Score 160.5; DB 1; Length 206; 47.7%; Pred. No. 0.00025; tive 9; Mismatches 35; Indels 13.
                       Actinopterygii, Neopterygii, Teleostei, Buteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 VKKPA--AAAK---KAAKSPKK---ATKAAKPKAAKPKAAKPKAAPKK 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACETYLATION (BY SIMILARITY)
100 GLOBULAR.
20672 MW; 72C440798066716C CRC64;
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Last annotation update)
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Pfam; PF00538; linker histone; 1.
ProDom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=85264847; PubMed=6443128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H15_HUMAN STANDARD; 1
P16401; Q14529; 01-AUG-1990 (Rel. 15, Created)
16-OCT-2001 (Rel. 40, Last sequincoct-2001 (Rel. 40, Last sequincoct-2001 (Rel. 40, Last annumental)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X02624; CAB37646.1; -.
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206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                        NCBI_TaxID=8022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
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MOD RES
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H15_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 40-113.

MEDLINE=94032251; PubMed=8218199;
Cerf C., Lippens G., Muyldermans S., Segers A., Ramakrishnan V.,
Wodak S.J., Hallenga K., Wyns L.;
"Homo- and heteronuclear two-dimensional NMR studies of the globular
domain of histone H1: sequential assignment and secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 SKKPGEVKEKAPKKKASAAKPKKPAAKKPAAAKKPKAVAVKKSPKKAKRPAASATKKS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKAEKAYAKKAKAKEKK-----AYAKKEAKAYKAAEAKKKAKAEAKKYAKEA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                          Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;
Characterization of the chicken histone H1 gene complement.
Generation of a complete set of vertebrate H1 protein sequences.";
J. Biol. Chem. 262:9656-9663(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 32:11345-11351(1993)
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.4%; Score 163; DB 1; Length 224;
llarity 43.8%; Pred. No. 0.00019;
Conservative 13; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACETYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22397 MW; D3D057CB97865CAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncorhynçhus mykiss (Rainbow trout) (Salmo gairdneri).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: Nuclear.
  01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 06, Created)
(Rel. 06, Last sequence update)
(Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001386; Histone H1/H5. Pfam; PF00538; linker histone; 1. ProDom; P0000373; Linkerhist_N; 1.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=87250632; PubMed=3597432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M17019; AAA48789.1; -. PIR; B28456; B28456.
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                       15-JUL-1999 (Rel. 38, Lar
Histone Hl.11L.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDB; 1GHC; 31-AUG-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                        NCBI_TaxID=9031;
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01-JAN-1988
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15-JUL-1999
Histone Hi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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H1_ONCMY
ID__H1_ON
AC PO635
DT 01-JA
DT 15-JU
DE H18CO
OS ONCOX
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Gaps

13;

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H11R CHICK
P08288;
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                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb=sib.ch).
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5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAA-----EAKKKAKAKAEAKKYAKEAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium smegmatis.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 700084 / mc(2)155;
MEDLINE=99110209; PubMed=9894918;
Lee B.H., Muruqaau-0ei B., Dick T.;
"Upregulation of a histone-like protein in dormant Mycobacterium
                        Albig W., Meergans T., Doenecke D.; "Characterization of the H1.5 gene completes the set of human H1
                                                                                                                                                                                                     Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   092HC5;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 0 ACETYLATION.
1 1 MISSING (IN REF. 1).
225 AA; 22449 MW; 26CD4A1E5D463CDA CRC64;
                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.9%; Score 160.5; DB 1
46.8%; Pred. No. 0.00027;
tive 7; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 AA
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  MEDLINE=97183654; PubMed=9031620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X83509; CAA58498.1; -. EMBL; Z98744; CAB11421.1; -.
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Genew; HGNC:4719; H1F5.
MIM; 142711; -
                                                                                                     Gene 184:141-148(1997).
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Best Local {
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Gen. Genet. 260:475-479(1998).
FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Histone Hi.11R.
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 АҚҚААҚҚАР---АҚҚАААҚҚТАТҚААҚҚАРАҚҚАА----ТҚАРАҚҚААТК-АРАҚҚАА 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAKAEAKKYAKEAAKAKEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87250632; PubMed=3597432;
Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;
Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;
Characterization of the chicken histone H1 gene complement.
Generation of a complete set of vertebrate H1 protein sequences.";
J. Biol. Chem. 262:9656-9663(1987).
-!- FUNCTION: H1STONES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLUIAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO00119; Bac_DNabind.

InterPro; IPRO00119; Bac_DNa binding; 1.

ProDom; PD001094; Bac_DNabind; 1.

SMART; SM00411; BHL; I.

PROSITE; PS00045; HISTONE LIKE; 1.

DNa-binding; DNA condensation; Repeat.

BOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.8%; Score 160; DB 1; Length 208; 54.3%; Pred. No. 0.00027; cive 3; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEGENERATE REPEATS REGION. CASFS77F61F7EF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 TKAPAKKAATKAPA-KKAAAKAPAKKA----ATKAPAKKAAAKKA 201
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(Rel. 08, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF068138; AAD13809.1; -. HSSP; P02346; 1HUU.
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01-AUG-1988
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Search completed: March 10, 2003, 12:17:11 Job time: 25.8354 secs
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                                                                                                                                                                                                                                                                                                                                                            109 SKKPGEGLEKAPKKKASAAKPKKAAAKKPAAAKKPKAAVAVKKSPKKAKPAASATKKS 168
                PIR; C28456; C28456.
HSSP P08287; CHC.
PinterPro; IPR001386; Histone H1/H5.
Probom; PD00338; Linker histone; 1.
Probom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
INIT_MET 0 0
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MEDLINE-9200931; PubMed=1916825;
Albig W., Kardalinou E., Drabent B., Zimmer A., Doenecke D.;
"Isolation and characterization of two human H1 histone genes within
                                                                                                                                                                                                                                                                                                                     1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKK---EAKAYKAAEAKKKAKAEAKKYAKEAAKAK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryora, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. VCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clusters of core histone genes.";
Genomics 10:940-948(1991).
-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANEOUS: THIS VARIANT ACCOUNTS FOR 60% OF HISTONE H1.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                  / Match 30.7%; Score 159.5; DB 1; Length 218; Local Similarity 47.7%; Pred. No. 0.0003; hes 52; Conservative 11; Mismatches 41; Indels 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                          218 AA; 21672 MW; CB9724BFF14654A6 CRC64;
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01-WAR-1989 (Rel. 10, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Histone H1.4 (Histone H1b).
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MEDLINE=87057092; Pubmed=3782055;
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J. Biochem. 100:359-368(1986).
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EMBL; M17020; AAA48790.1;
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PIR; C40335; C40335.
HSSP; P08287; IGHC.
Genew, HGNC: 4718; HIF4.
MIM; 142,200.
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P10412;
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                      Pfam; PF00538; linker histone; i.
Probon; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
Acceylation; Methylation.
INIT_MET 0 0
MOD_RES 1 1 ACETYLATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KKYAKKAEKAYAKKAKAAKEKK--AYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKE 59
                                                                                                                                                                                                                                                                                                                              Length 218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 AKKAKSPKKAKARAKPKKAPKSPAKAKVKPKAAKPKTAKPKAAKPKKAA 214
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48.6%; Pred. No. 0.00038;
Live 7; Mismatches 43; Indels
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25 25 METHYLATION (PARTIAL).
35 113 GLOBULAR.
218 AA; 21734 MW; E210BEC152ABE882 CRC64;
InterPro; IPR001386; Histone H1/H5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES

Ogywx1 pseudomonas Ogt5c8 plasmodium O8x5c5 escherichia O8x8c1 salmonella O8x8c1 salmonella O8x8c2 yersinia pe O8xwn7 ralstonia s O9cm70 pasteurella O61164 plasmodium O139576 chlamydomon O1395 drosophila O84528 paramedium O95s18 drosophila O84528 paramedium O95s18 drosophila 2937k4 erwinia chr Description 0937X4 09WX1 08X95 08X965 08X8C1 08Z8C1 08Z8C2 08Z8C1 09CXVN7 Query Match Length DB 202 190.5 1180.5 1184.5 1181.5 178 178 176.5 170.5 170.5 170.5 166.5 166.5 164.5 164.5 Score

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Result

Q26947 trypanosoma Q9kr10 vibrio chol Q9ar18 lens culina Q9ar20 pisum sativ Q9ar21 lathyrus sa Q9ar22 lathyrus sa Q9ar22 pisum sativ Q9ar23 pisum sativ Q9ar23 pisum sativ Q9ar23 pisum sativ Q9ar24 pisum condium Q9ar24 pisum condium Q9ar24 pisum condium Q9ar24 pisum condium Q9ar24 pisum ac Q5ar24 pisum condium Q9ar24 pisum condium C9ar24 pisum condium co	update) update) un update) un ipdate) un; Enterobacteriaceae; zaroni J.; iemi tol-pal genes."; bDBJ databases.	tch al Similarity 41.3%; Score 202; DB 2; Length 395; al Similarity 41.3%; Pred. No. 2e-06; 62; Conservative 15; Mismatches 32; Indels 22; Gaps 4; AKKYAKRAEKAYAK
26 5 Q26947 26 16 Q9KR10 27 10 Q9KR20 28 10 Q9KR20 29 10 Q9KR20 20 10 Q9KR21 20 10 Q9KR21 20 10 Q9KR21 20 10 Q9KR27 21 10 Q9KR27 22 10 Q9KR27 23 10 Q9KR27 24 13 Q90KR27 25 10 Q9KR27 26 10 Q9KR27 27 10 Q9KR27 28 10 Q9KR27 29 16 Q9KR27 20 10 Q9KR27 20	ALIGNMENTS  19, Created) 19, Last sequence 19, Last annotation 19,	38.9%; Score 202; DB 2; Length 395; 47.3%; Pred. No. 2e-06; ive 15; Mismatches 32; IndelsKAKAKEKKAYAKEAKAYKAAEAKKAK
162.5 11.3 1128 161.5 31.2 356 161.5 31.1 295 161.5 31.1 295 161.5 31.1 295 161.5 31.1 297 161.5 31.1 297 161.5 31.1 297 161.5 31.1 297 160.5 30.9 301 158 30.4 290 158 29.8 30.4 290 154.5 29.8 30.4 290 154.5 29.8 289 154.5 29.6 275 150 28.9 289 148.5 28.6 275 146.5 28.1 291 146.5 28.1 291 146.5 28.1 291 146.5 28.1 293 146.5 28.1 293 146.5 28.1 293 146.5 28.1 293 146.5 28.1 293 146.5 28.1 293 146.5 28.1 293	137K4 PRELIM 137K4; -DEC-2001 (TEMB 1-DEC-2001 (TEMB 1-DA Protein. 10A. 10A. 10A. 10A. 10A. 10A. 10A. 10A	Ma 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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"Evolutionary relationships of conserved cysteine-rich motifs in
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Q8X965;
01-MAR-2002 (
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"The Pseudomonas putida peptidoglycan-associated outer membrane
lipoprotein (PAL) is involved in maintenance of the integrity of the
cell envelope.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 K--AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
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"Characterization of an Opri null mutant of Pseudomonas putida.";
J. Bacreriol. 178:5836-5840(1996).
EMBL; X74218; CAB50780.1;
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                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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VOTI_TaxID=5855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ramos-Gonzalez I.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodriguez-Herva J.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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PRINTS; PR00624; HISTONEH5.
SEQUENCE 372 AA; 40133 MW; 87F49785ECC3C0BC CRC64;
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Last annotation update)
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Michon P., Stevens J.R., Kaneko O., Adams J.H.;
                                                             372 AA.
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Bacteriol. 178:1699-1706(1996)
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MEDLINE=96422022; PubMed=8824639;
                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20,
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 59; Conserv
                                                                                                                                                                                                                                                                  Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=303;
                                                                                                                                                                                                          Tola protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MT-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                         09WWX1;
                                                          Q9WWX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8T5C8
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RESULT 2
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                           Q9WWX1
                                                                HDD THE LEAD OF THE LAND OF TH
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1262 АККАЕЕ--АRКАЕБААККАЕБААККАЕЛАККАЕЛАЯККАЕЛАККАЕБАККАЕБАRКАЕЛ
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STRAIN=LT2 / SGSC1412 / ATCC 700720;

STRAIN=LT2 / SGSC1412 / ATCC 700720;

MEDLINE=21534948; PubMed=11677609;

MCDIalland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                        51 KEAAKAKKBAYKAEAKKYAKAKAKEYKEYAAAEAKKAEAAK----AYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 EAYK--AEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAK---AAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                    Length 1866;
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                      CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
adhesive molecules of malaria parasites.";"
Mol. Biol. Evol. 0.0-0(2002).
EMBL, AV4042083; AAL10508.1; SEQUENCE 1866 AA, 212420 MW; DC692D7CFAE7D93F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.5%; Score 184.5; DB 16;
55.5%; Pred. No. 3e-05;
Micmarches 25;
                                                                                                                                                 Query Match 36.7%; Score 190.5; DB 5; Best Local Similarity 49.6%; Pred. No. 4.7e-05; Matches 61; Conservative 17; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
                                                                                                                                                                                                                                                                   5 AKKAEKAYAKKAKAAKE----KKAYAKKEAKAYKAAEAKKKA
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InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREBZEI.
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Yersinia pestis
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Best Local Simi
Matches 63;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 5:47 / RIMD 0509952;

MEDINRE-21156231; PubMed-211258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Ruhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

IDNA Res. 811-22(2001).

REMBL; AR005523; BAB341971; -.

REMBL; AR0005531; BAB341971; -.

REMBL; AR00308; ANTIFREEZEI.
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                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=O157:H7 / EDL933 / ATCC 700927;

MEDLINES-21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L.,

Grocbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

"Genome sequence of entror R.R.;

"Genome sequence of entror and the control of the 
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Membrane spanning protein, required for outer membrane integrity
(Membrane spanning protein TolA).
TOLA OR Z0907 OR ECS0774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 AKKEAY-KAEAKKYAKAAKAEKKEYAAAEAKK---AEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 394;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 60; Conservative
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NCBI_TaxID=601;
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STY0793.
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Q8Z8C1;
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MEDLINE-21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.E.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Yersinia pestis, the causative agent of plague.";
Mature 413:251-527(2001).
BMBL, AJ414146; CRG89566.1; -
InterPro; IPRO0104; Antifreeze 1.
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Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
Whitehead S., Barrell B.G.;
                                                                                        "Complete genome sequence of a multiple drug resistant Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                               34.3%; Score 178; DB 16; Length 376; 52.3%; Pred. No. 7.4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                      376 AA; 38804 MW; EC21F2C4767A8A42 CRC64;
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10; Mismatches
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                                                                                                                  enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
EMBL, AL667268; CAD05209.1; -.
PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01574; TUBBYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / BIOVAR ORIENTALIS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            58; Conservative
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                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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SEQUENCE 388 AA
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InterPro; IPR000533; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
Complete protecome.
SEQUENCE protecome.
SEQUENCE A89 AA; 42197 MW; B4032F2A2FD9E94B CRC64;
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HSSP; P19934; 1TOL
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01-MAR-2002 (
Histone H1.
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01-OCT-2000
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Max B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
Complete genomic sequence of Pasteuralla multocida Pm70.";
Proc. Natl. Acod Sci. 05 A. 98:3460-3465(2001).
EMBL; Ano6136-3 AAK03052.1;
                                                                                                                                                                                                                                                          Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Fenard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Meissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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Pasteurella.
                                                                                                                                               Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 AA; 19279 MW; D3831B590510272D CRC64;
                                                                           01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last sequence update)
Last annotation update)
                                                    200 AA
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                                                    PRT;
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MEDLINE=21681879; PubMed=11823852;
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InterPro; IPR00104; Antifreeze_1.
InterPro; IPR00393; treacle.
PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01503; TREACLE.
                                                                                                                      Probable histone H1 protein. RSC2793 OR RS00453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.0%;
Best Local Similarity 54.5%;
Matches 67; Conservative
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                                                    PRELIMINARY;
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SEQUENCE 200 AA;
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                                                    08XVN7
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                         RESULT 8
Q8XVN7
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Q9CM70
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SEQUENCE FROM N.A. MEDLINES 962390479; MEDLINES 96120866; PubMed-8590479; Fabry S., Muller K., Lindauer A., Park P.B., Cornelius T., Schmitt R.; The organization structure and regulatory elements of Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1205 AKKAEEE-RKKAEAVK-KAEEAKKKAEBAKKAEERKK-KAEAAKKALERKKKSEAAKKAL 1261
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Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                              57 KKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                  Length 1701;
  DB 16; Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=YM;
MEDLINE=98115903; PubMed=9448314;
Kappe S.H.I., Noe A.R., Fraser T.S., Blair P.L., Adams J.H.;
A family of chimeric erythrocyte binding proteins of malaria parasites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium yoelii yoelii.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
                                                                                         6 KKAEKAYAKK-AKAAKEK-KAYAKKEAKAYKAAEAKKKAKA--EAKKYAKEA
Query Match 33.4%; Score 173.5; DB 16; Lengtl:
Best Local Similarity 48.7%; Pred. No. 0.00015;
Matches 55; Conservative 18; Mismatches 31; Indels
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Best Local Similarity 53.5%; Pred. No. 0.00091;
Matches 54; Conservative 11; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 95:1230-1235(1998).
EMBL; AF031886; AAC05366.1; -.
SEQUENCE 1701 AA; 199268 MW; EDA8E2DEFD87CE8A CRC64;
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Last annotation update)
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20,
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FAU OR ČG6544.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 OKAAEEAKALKAAEDAAOKAAEEARLAEEAAAOKVAEEAAQKAAEEARLAEEAAAOKAAE 450
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MEDIJES-219224; PubMed=1731966;
MEDIJES-219224; PubMed=1731966;
MARATCHUK W.W., Muller F.W., Beck C.F.;
"Two GC-rich DNA elements of Chlamydomonas reinhardtii with complex arrangemente of directly repeated sequence motifs.";
Plant Mol. Biol. 18:143-146(1992).
EMBL; X17208; CAA35080.1; -.
                                                                                                                                                                                                                                                              STRAIN-BERKELEY;
Stapleton M., Broketein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AX060997; AAL28454.1; -.
SINBBL, AX060997; AAL28454.1; -.
SINBBC, EBRDO020439; fau.
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.1%; Score 166.5; DB 5; Length 619; 41.0%; Pred. No. 0.00067; ive 16; Mismatches 30; Indels 33;
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                                                                       (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 20, Last annotation update)
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Last annotation update)
                                                      Created)
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01-NOV-1996 (TrEMBLrel. 01, La
01-DBC-2001 (TrEMBLrel. 19, La
CGCr-4 product (Fragment).
                                                      (TrEMBLrel. 19,
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tes 55; Conservative
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                    PRELIMINARY;
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EAAQKAAEEAALKA 464
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01-DEC-2001 (
01-MAR-2002 (
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                    Q95S18
Q95S18;
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Q39598
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                                                                                                                                                                                                                                                                                                                                                        Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKAEKAYAKK--AKAAKEKKAYAKKEAKAYKAAEAKKKAK-AEAKKYAKEAAKAK 57
                                                                                                                                                                                                                                                                2 KKYAKKA---EKAYAKKAKAKEKKAYAKKEA----KAYKAAEAKKKAKAEAKKYAKEA-
histone genes reveal features linking plant and animal genes.";
Curr. Genet. 28:333-345(1995).
                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 KEAYKAEAKKYAKAAKAEKKEYAAAEAKK-AEAAKAYKAEAAKAAAKEAAYE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY
                                                                                                                                                                                              Length 232;
                                                                                                                                                                                          Query Match
32.8%; Score 170; DB 10; Length 2:
Best Local Similarity 46.3%; Pred. No. 0.00016;
Matches 57; Conservative 10; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Neesen J., Heinlein U.A.O., Buenemann H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION FOSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL
                                                                InterPro; IPR001386; Histone H1/H5.
InterPro; IPR003216; LinkerhIst_N.
Pfam; PP00538; Linker histone; I.
ProDom; PD000373; Linkerhist_N; I.
SMART; SM00526; H15; I.
SEQUENCE 232 AA; 24693 MW; 2D006AE44A8FA037 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AE]-X.
76BAA7B2A2DF732C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.7%; Score 169.5; DB : 48.2%; Pred. No. 0.0002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Axoneme-associated protein MST101(3). MST101(3) OR DHMST101. Drosophila hydei (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [AE]
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                                  U16726; AAA98452.1; -. P02259; 1HST.
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001395
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4

Indels 33; Gaps

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5
                                      Gaps
                                                                           ---YAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEA 46
                                                                                                18;
31.6%; Score 164; DB 10; Length 265; 39.4%; Pred. No. 0.00045; tive 21; Mismatches 38; Indels 1
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RESULT 13

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47 KKYAKBAAKAKKEAYKAEAKKYAKAAK----AEKKEYAAAEAKKAEAAKAYKAEAAKAAA 102
                                             79 AEAKAKEADEARAAEAEARAVAEAWAAAEAEARAEAEAWAAAEAEAWAAAEVEARAAQA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20478054; PubMed=11021991;
Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
"Characterization of a beta-1,3-glucanase encoded by chlorella virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE PROM N.A.
MEDLINE=20013326; PubMed=10544099;
Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
Lisec A.D., Nickerson K.W., Van Etten J.L.;
"Chlorella virus PBCV-1 encodes a functional homospermidine
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=96187795; PubMed=8614977;

Lu Z., Li Y., Que Q., Kutish G.F., Rock D.L., Van Etten J.L.,

Lanalysis of 94 kb of the chlorella virus PBCV-1 330-kb genome: map
posttions 88 to 182.";

Virology 216:102-123(1996).
                                                                                                                                                                                                                                                                                                 Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
NCBI_TaxID=10506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Gurnon J.R., Graves M.V., Van Etten J.L.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, 142580; AAC96576.1; -.
IntqrPro; IPRR02048; EF-hand.
PROSITE; PSO0018; EF HAND; UNKNOWN 1.
SEQUENCE, 311 AA; 35390 MW; 9780E9882AFEF88A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                             311 AA.
                                                                                                                                                                                             PRT;
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                                                                                                                                                                                             PRELIMINARY;
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Submitted (MAY-1997)
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Submitted (SEP-1997)
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Submitted (DEC-1995)
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                                                                                       103 KEAAYEA 109
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199 EAKAKEA 205
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SEQUENCE
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Q84528;
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Search completed: March 10, 2003, 12:25:59 Job time : 58.7194 secs

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March 10, 2003, 12:15:01; Search time 56.7996 Seconds (without alignments) 255.712 Million cell updates/sec
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:
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GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908470 seqs, 133250620 residues
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Listing first 45 summaries
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519
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Perfect score:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Copolymer molecula	Copolymer molecula	Copolymer molecula	Copolymer molecula	Recombinant copoly	Recombinant copoly	Copolymer molecula	Peptide #10 used i	Amino acid polymer	Poly-Lys-Ala used
SUMMARIES	AAY82577	AAY82576	AAY82575	AAY82574	AAR06445	AAR06446	AAY82573	AAY98499	AAY59044	AAU04289
DB	21	21	21	21	11	11	21	21	21	22
% Query Match Length DB	109	98	77	99	154	106	99	100	100	100
% Query Match	100.0	60.2	55.7	44.0	40.3	36.0	34.8	34.6	34.6	34.6
Score	519	312.5	289	228.5	209	187	180.5	179.5	179.5	179.5
Result No.	-	~	e	4		9	7	80	6	10

Nucleic acid trans Amino acid sequenc Trypanosoma cruzi Histone Hi isoform Human histone Hi 5 Human histone Hi 1 Human histone Hi i	Histone H1-4, frag Human linker histo Trypanosoma cruzi Human histone H1 i Human histone H1 i Trypanosoma cruzi Pentide fragment o	Human linker histo Quail H1 histone p Human histone H1 Human histone H1 Human histone H1 Human histone H1 Drosophila melanog Plasmodium yoelli Synthetic helical	Drosophila melanog Adhesive polypepti Antibiotic potenti (Lys) 434 protenti (Lys) 434 protein s M. tuberculosis hi M. tuberculosis hi Listeria monocytog Peptide #8 used in Anino acid polymer Poly-L-Lysine used Nucleic acid trans Peptide #2951 enco
AAB45852 AAY14928 AAR84568 AAY34068 AAY34060 AAY34060	AAU09944 AAR13234 AAR84569 AAW29477 AAX34034 AAX57332 AAR1099456	AACS 945 AAX76981 AAX29476 AAX34033 AAX57331 AAB2173 AAB2128 AAR25206	ABB63276 AAW31829 AAW31821 AAY36903 AAY34055 AAY34055 AAY34053 AAY390427 AAY89042 AAU98437 AAB45850
200000000000000000000000000000000000000	2001 2001 2001 2001 2001 2001 2001 2001	222223232323	22 22 23 23 25 25 25 25 25 25 25 25 25 25 25 25 25
100 643 158 158 226 226	2334 2122 2122 2138 2188 264	130 222 222 222 607 1507	299 4431 221 4444 1000 1000 1000
3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	0000000	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	28.1 27.1 27.1 27.1 27.1 28.1 29.1 20.1 20.1 20.1 20.1 20.1 20.1 20.1 20
179.5 178 162.5 160.5 160.5 160.5	159.5 158.5 158.5 158 158 158	154.5 152.5 152.5 152.5 152.5 151 148.5	146 144 144 144 143 141.5 141 141 141 138.5
111 112 113 114 116	118 222 223 24 24 25 25 26 27	33310088469	3 3 3 3 3 3 3 3 3 3 3 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

RESULT 1
AAY82577

ID AAY82577

ID AAY82577

ID AAY82577

ID AAY82577;

XX

AAY82577;

XX

AAY82577;

XX

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7.

XX

Copolymer molecular weight marker; TV-marker; immune disease;

XM

Copolymer; molecular weight marker; TV-marker; neuroprotective;

XM

Copolymer acctate; autoimmune disease; antiarthritic; neuroprotective;

XM

Copolymer; molecular weight marker; TV-marker; immune disease;

XM

Copolymer; molecular weight marker; TV-marker; neuroprotective;

XM

Copolymer; molecular weight marker; TV-marker; immune disease;

XM

Accolute; immunosuppressive; antiarthrimanatory

Accolute; immunosuppressive; demyelinating disease; osteoarthritis;

XM

Crohn's disease; chronic immune thrombocytopaenia purpura; colitis;

XM

Accolute; disease; disease; disease; dillain-Barre's syndrome; psoriasis;

XM

Mo20018794-A1.

XX

PD

CAPR-2000.

XX

YESP-1999; 99WO-US22402.

XX

YEBR

ZE-SEP-1999; 99WO-US22402.

XX

YEBR

YEBP

06-APR-2000.

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for and an amino acid composition are used as molecular weight markers for all tramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune claimed for treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple clares in the material autoimmune opporating, autoimmune thyroiditis, autoimmune benevolating, autoimmune thyroiditis, autoimmune veceranitis, contact sensitivity disease, diabetes mellitus, Graves purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, myasthenia gravis, psortiasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graff disease, graff-versus-service defined molecular weights and physpetides of the invention have defined molecular weights and physpetides of the invention have analogous to analogous to a disease.
                                                                                                                                                                                                               Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   molecular weight markers.
                                                                                              WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AA;
Lis D;
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Gad A,
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Gaps 1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKKEA 60 . 0 100.0%; Score 519; DB 21; Length 109; 100.0%; Pred. No. 1.4e-36; Indels 100.0%; Pred. .... Conservative Best Local Similarity Matches 109; Conserv Query Match ઠે

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1 AKKYAKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60 61 УКАЕАККҮАКААКАЕККЕУАААЕАККАЕААКАУКАЕААКАААКЕААУЕА 109 g ઠે

61 УКАЕАККУАКААКАЕККЕУААВЕАККАЕААКАУКАЕААКАААКЕААУЕА 109

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AAY82576 standard; peptide; 86 AA

RESULT 2

AAY82576;

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.

Copolymer; molecular weight marker; TV-marker; immune disease; glalitramer accetate; autolmmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antichyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidiabetic; thyromimetic; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatory darthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; dulliain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. AAY82576
XX
AC
AC
AAY8
XX
XX
DE
COPC
XX
XX
XX
XX
XX
XX
AD
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XX
AD

Unfidentified

WO200018794-A1

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular eight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for all composition are used as molecular weight markers for golypeptides of the invention are used as molecular weight markers for used for treating and preventing immune diseases in a mammal. Autoimmune completed include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple calerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinits, Crohn's disease, formic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, duillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriaais, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                            Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKK-EKAYAKKA-----EKAAKKAEAKAYKAAEAKKKA------36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKKKEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YKAEAKKYAKAAKAEKKEYAAAEAK-KAEAA-KAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.2%; Score 312.5; DB 72.1%; Pred. No. 2e-19; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 14; 72pp; English.
                                                                                                                                                             CO LTD.
                                                                                                              98US-0101693.
                                                                  99WO-US22402.
                                                                                                                                                             (YEDA ) YEDA RES & DEV CO L
(TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80; Conservative
                                                                                                                                                                                                                                                                                WPI; 2000-317499/27.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 AA;
                                                                                                                                                                                                                                    Lis D;
                                                                  24-SEP-1999;
                                                                                                                25-SEP-1998;
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                                                                                                                                                                                                                                 Gad A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
d
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Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; hamemestatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5. AAY82575 standard; peptide; 77 AA. 28-JUL-2000 (first entry) AAY82575; RESULT 3

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28-JUL-2000 (first entry)

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflamatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic mannals, autoimmune opophoritis, autoimmune thyroiditis, autoimmune uvecretinitis, contact sensitivity disease, diabetes mellitus, Graves cuites, contact sensitivity disease, diabetes mellitus, Graves contact sensitivity disease, diabetes mellitus, contact sensitivity disease, diabetes mellitus, contact sensitivity disease, dispense, dialopathic mannals and contact sensitivity disease, dispense, dispense dialopathic mannals and contact sensitivity disease, dispense, dispense dialopathic mannals and contact sensitivity dispense dialopathic mannals an inflammatory condition; multiple sclerosis; rheumatoid arthritis; cothn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersenativity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases pemphigus vulgaris; systemic lupus erythematosus. Claim 10; Page 14; 72pp; English (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC. 98US-0101693. 99WO-US22402. molecular weight markers WPI; 2000-317499/27. WO200018794-A1 Gad A, Lis D; 25-SEP-1998; Unidentified 24-SEP-1999; 06-APR-2000. 

77 AA; Sequence

4. Gaps 9 1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKA------36 1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 32; Score 289; DB 21; Length 77; Pred. No. 1.6e-17; 1; Mismatches 3; Indels ... 55.7%; 셤 ઠ

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AAY82574 standard; peptide; 66 AA. AAY82574; AAY82574
ID AAY8
XX
AC AAY8 RESULT 4

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidamenic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; diopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases Copolymer molecular weight TV-marker amino acid seguence SEQ ID NO:4. (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC. 99WO-US22402. 98US-0101693. WPI; 2000-317499/27. WO200018794-A1 Lis D; Unidentified 24-SEP-1999; 25-SEP-1998; 06-APR-2000 Gad A, 

weight TV-marker polypeptides from the present invention. The present weight TV-marker polypeptides from the present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for and an amino acid composition are used as molecular weight markers for used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, crohn's disease, foronic immune thyroiditis, autoimmune uveoretinitis, crohn's disease, choosic immune thyroiditis, draves disease, diabetes mollitus, Graves disease, duillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriaais, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayde-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as Claim 10; Page 14; 72pp; English.

66 AA; Sequence

Gaps 43; 44.0%; Score 228.5; DB 21; Length 66; 56.9%; Pred. No. 1.6e-12; Indels 0; Mismatches 62; Conservative Local Similarity Query Match Best Loca Matches

4

25

1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKKKEA 60 1 AKKYAKK-EKAYAKAKKA-----EAKAAKKA-----

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61 УКАЕАККҮАКААКАЕККЕУАААБАККАЕААКАҮКАЕААКАААКБААУБА 109

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90US-0473845.
89US-0312541.
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                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
            92 AYKAEAAKAAAKEA 105
                                 142 KYKKEAEK--AKEA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunological activity
                                                                                                                                                                                                                                                                                                                                                              (REPL-) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1990-255848/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                certain amino acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also AAQ05664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ06446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fusion protein.
                                                                                                                                                                                                                                                                                                      16-FEB-1990;
                                                                                                                                                                                                                                                                                                                            07-FEB-1990;
                                                                                                                                                                                                                                                                                                                                       17-FEB-1989;
                                                                                                                                         03-JAN-1991
                                                                                                                                                                                                                                                                               22-AUG-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
                                                                                                                                                                                                                                                        EP383620-A.
                                                                                                                                                                                                                                   Synthetic
                                                                                                                  AAR06446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                    Cook KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                AAR06446
            8
                                셤
                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRLE B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences.

A mechionine residue occurs between the Protein A and rCOP-1 sequences. C. the COP-1 polypeptide may be cleaved from the fusion protein.

COP-1-77 contains oligonucleotide duplexes incoding the following segments: YKK, BEX, KAK, AAK, and AAA. The N-terminal alarine residue crophalomyelitis. They are used to prevent, arrest or control a encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair or are products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 EYKKKARAABABESKKBABEBABYKKYKKKAKAKYKKKAKBABKARAABABABKAKBABY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 KKKAKEAEKAKKAKYKKYKKEAEAAKAAKAAAAAAAYKKEAEA--AAEAEKAKYKKKAKEA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKYAKKAEKA-----YAKKAKAAKEKKAYA----KKEAKAYKAAEA-----KKKAK-A 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 EAKKYAKEAAKA--KKEAYKAEAKKYAKAAKAEK-----KEYAAAEAKKAEAA--K 91
                                                                                                                                                                                                                                                                                                                                                                                                        Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity
                                                                                                                                                   Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 154;
                                                                                                                          Recombinant copolymer 1-77, myelin basic protein analogue.
26 -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 209; DB 11;
Pred. No. 1.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
                                                       AAR06445 standard; protein; 154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 11; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.78;
                                                                                                                                                                                                                                                                                        90US-0473845.
89US-0312541.
                                                                                                                                                                                                                                                                    90EP-0301700
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 53.7*
Local 72; Conservative
                                                                                                                                                                                                                                                                                                                          (REPL-) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-255848/34.
                                                                                                                                                                           multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 AA;
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                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ05664.
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                                                                                                                                                                                                                                                                                         07-FEB-1990;
                                                                                                      03-JAN-1991
                                                                                                                                                                                                                                          22-AUG-1990
                                                                                                                                                                                                                      EP383620-A.
                                                                                                                                                                                                Synthetic.
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                                                                               AAR06445;
                                                                                                                                                                                                                                                                                                                                                 Cook KS;
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                                            RESULT 5
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To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NoV-1984 US491009, NRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences. the COP-1 polypeptide may be cleaved from the fusion protein. the COP-1 polypeptide may be cleaved from the fusion protein. CCOP-1-19 contains oligomucleotide duplexes incoding the following segments: YKK, AAE, KAK, KRA, RAA, AKA KEA, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKAAEKAKAAK-KAYEAEKAKAKYEAK----- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              АККАЕКАУАККАКАХААКЕККАУАККЕАКАУКААЕАКККАКАЕАККУАКЕААКАККЕАУКАЕ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                  Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing genes encoding random polymers of aminoacid(s) - i producing recombinant polypeptide(s) with biological and/or
                                                                                                                                                                                                                                                                                                Recombinant copolymer 1-19, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.0%; Score 187; DB 11;
55.0%; Pred. No. 7.7e-09;
tive 11; Mismatches 20;
AAR06446 standard; protein; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 12, 25pp, English.
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56 AA;

Sequence

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glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; chronic immune thrombocytopeania purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                     Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copolymer; molecular weight marker; TV-marker; immune disease;
65 AKKYAKAAKAEKKEYAAAEAKKAEAA----KAYKAEAAKAAAK-EAAYE 108
                              pemphigus vulgaris; systemic lupus erythematosus
                                                                                                                                                                                                                   AAY82573 standard; peptide; 56 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US22402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0101693.
                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200018794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lis D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-2000.
                                                                                                                                                                                                                                                                                      AAY82573;
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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight markers for glatifamer acetare related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include archritic conditions, antibody-mediated diseases and inflammatory conditions, e.g. multiple clerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune ophoritis, autoimmune thyroiditis, autoimmune vophoritis, autoimmune thyroiditis, autoimmune thyroiditis, autoimmune thyroiditis, autoimmune thyroiditis, autoimmune thyroiditis, outsil a propara, colitis, contact sensitivity disease, diabetes mellitus, Graves urpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's synfrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and cellayed-type hyperespitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to constant the superparties and physical properties which are analogous to a prince as an acetare molecules, which makes them ideal for use as
                                                                                                                                                      AAY82571 to AAY82577 represent specifically claimed copolymer molecular
Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecular weight markers.
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The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36633-A36652 and peptide sequences AAY98456-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transgenic animals (as models for human carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from endosomes, without requiring endosomal or lysosomal
                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent
                                          Gaps
                                                                           1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKKKA 60
                                                                                                                                                                                                                                                                                                                                                                                                                               Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
                                        53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.6%; Score 179.5; DB 21; Length 100;
   Score 180.5; DB 21; Length 56;
Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith LC;
                                                                                                                                                  61 YKAEAKKYAKAAKAEKKEYAAAEAKKABAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                    -----YKABAKKAAKBA 56
                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Peptide #10 used in nucleic acid transporter system.
                                                                                                1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKAEAK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WOO SLC,
                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 125-128; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sottchalk S, Sparrow J, Cristiano RJ,
                                                                                                                                                                                                                                                                                 AAY98499 standard; Peptide; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BAYU ) BAYLOR COLLEGE MEDICINE.
34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-0167641.
                                                                                                                                                                                                                                                                                                                                                          31-JUL-2000 (first entry)
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-281993/24.
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-DEC-1993;
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19-MAR-1993;
                                        50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                     AAY98499;
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                                        Matches
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ID AAY9
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Indels

DB 21; Length 100;

Score 179.5; DB 2 Pred. No. 3.1e-08; 8; Mismatches

34.6%; 55.6%;

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KAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKY 68
                                                                                                                                            69 AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                          Conservative
                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 AA;
                  100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAYU ) BAYLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6177554-B1
                                                                 55;
                                                                                                                                                                                                                                                                                   23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WOO SLC,
                                                                                                                                                                                                                                                          AAU04289;
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                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety, that is capable of moving or initiating movement through a nuclear membrane; and or [6] a lysis moiety that enables the transport of the entire complex or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytolism of the cill. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an unimal model. The NTS can be used in vitro with tissue culture cells which allows the role of various nucleic acids to be studied by targeting specific expression into specifically targeted tissue culture cells. The lysis agent within the NTS avoids the problem of endosomal/lysosomal
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/note= "Lys-Ala in positions 3 to 100 may be optionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                  Gaps
                                         KAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKY 68
                                                         cytosis;
                                                                                                                                                                                                                                                                                 sport system; NTS; cell surface receptor; cytosi, lysis moiety; transgenic animal; human disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith LC;
               33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sparrow J,
                                                                                           AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                                                                                                                  60 AKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKA 98
     Pred. No. 3.1e-08;
                                                                                                                                                                                                                                                          Amino acid polymer seq ID NO: 64 of US5994109.
55.6%; Pred. .v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Columns 123-124; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gottchalk S,
                                                                                                                                                                                                                                                                                 Nucleic acid transport system; NTS;
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                              AAY59044 standard; peptide; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                         nucleic acid delivery; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0167641.
92US-0855389.
93WO-US02725.
93US-0167641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0460890.
                                                                                                                                                                                                                                 (first entry)
                 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-038262/03
     Best Local Similarity
                                                                                                                                                                                                                                                                                                nuclear membrane;
                                                                                                                                                                                                                                                                                                                                                            Key
Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAR-1992;
19-MAR-1993;
14-DEC-1993;
                                                                                                                                                                                                                                07-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                        US5994109-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degradation
                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                       AAY59044;
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               Matches
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                                                                                                                                                                                                                                                        Nucleic acid transport, cytosis; ligand; lysis agent, spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Lys-Ala in positions 3-100 may be present or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid transport system, useful for creating transgenic for assessing human disease such as cancer in an animal model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid into specific cells e.g. in gene therapy to dacid into hepatocytes, muscle cells or bone forming cells.
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Pred. No. 3.1e-08;
8; Mismatches 33; Indels
                                                                                                                                                                                                  Poly-Lys-Ala used in nucleic acid transporter system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Column 131, 111pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 3..100
AAU04289 standard; Peptide; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLLEGE MEDICINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-0855389.
93WO-US02725.
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                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-365933/38
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Best Local Similarity
Matches 55; Conserv
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This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nucleic acid and covalently linked to a nucleic acid and covalently linked to a nucleic acid the nucleic acid transporter system can also be used in a method con the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, and polypeptides, such as hormones, youth factors, enzymes, clotting factors, twmor suppressors, viral antigens, parasitic antigens, tumor antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems.
                                                                                                                                                                                                                                                                                                                                                                  growth factor, clotting factor, apolipoprotein, receptor, drug, oncogene, tumor antigen, tumor suppressor, viral antigen, parasitic antigen,
                                                                                                                                                                                                                                                                                                                                             Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme;
KAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKY 68
                      Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                                                                                                                                                                                                                                                                                                             Nucleic acid transporter system peptide ligand SEQ ID NO 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WOO SLC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith LC,
                                                                         AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEAA 106
                                                                                              60 AKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Column 125-126, 105pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cristiano RJ,
                                                                                                                                                                                                  AAB45852 standard; Protein; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-0167641.
92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0460971
                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gottchalk S, Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-049093/06
                                                                                                                                                                                                                                                                                                                                                                                                    bacterial antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BAYU ) BAYLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-DEC-1993;
                                                                                                                                                                                                                                                                         21-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6150168-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-NOV-2000.
                                                                                                                                                                                                                                     AAB45852;
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ID AAB4
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The invention provides heat-killed Mycobacterium vaccae, or recombinant

M. vaccae proteins. The M. vaccae proteins may be employed to activate

T cells and natural Miler cells, to stimulate the production of

cytokines, to enhance the expression of co-stimulatory molecules on

dendritic cells and monocytes, and to enhance dendritic cell maturation

and function. The proteins can be expressed by standard recombinant

methodology. Pharmaceutical compositions comprising the proteins or

nucleic acid sequences encoding the proteins can be used for the

treatment, prevention, and detection of disorders including infectious

treatment are used for treatment of diseases of the respiratory system,

such as mycobacterial infections, asthma, allergies, tuberculosis,

leprosy, sarcoidosis and lung cancers, and disorders of the skin such as

psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,

alopecia areata, and skin cancers such as basal carcinoma, squamous cell
                                                                                                                                                                                                                                              Mycobacterium vaccae protein; antigen; T cell activation; cytokine; dendritic cell maturation; infectious disease; immune disorder; cancer; respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 178; DB 20;
Pred. No. 9.5e-08;
6; Mismatches 34;
 AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                 Amino acid sequence of M. vaccae antigen GV-45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Visser ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enhancing immune response to an antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tan P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                   ż
                                                                                                                                                                                                                                                                                                                                   squamous cell carcinoma; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 239; 243pp; English.
                                                                                                                AAY14928 standard; protein; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0996624.
97US-0997080.
97US-0997362.
98US-0095855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
34.3%;
Best Local Similarity 54.5%;
Matches 60; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-NZ00189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0205426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0156181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prestidge RL, Skinner MA,
                                                                                                                                                                                25-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carcinoma and melanoma
                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium vaccae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-430163/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ11393.
                                                                                                                                                                                                                                                                                                                                                                                                     WO9932634-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1997;
23-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1997
                                                                                                                                                 AAY14928;
 69
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                                                                                   RESULT 12
                                                                                                  AAY14928
ID AAY1
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Gaps

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33; Indels

8; Mismatches

55; Conservative

Matches

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Best Local Similarity

Query Match

34.6%; Score 179.5; DB 22; Length 100; 55.6%; Pred. No. 3.1e-08;

10 KAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKY 68

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8

57 KK--EAYKAEAKKYAKAKAEKKEYA---AAEAKKAEAAKAYK-AEAAKAAAKEAA 106

1 AKKYAKKAEKAYAKKAKAAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYA----KEAAKA 56

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ARR84565-R84569 are polypeptides of the TCR27 protein of T.cruzi

The proteins are all fusion products with glutathione-S-transferase

(GST) and some contain a linker sequence. The TCR27 protein comprises

a 95 amino acid (aa) N-terminal region; 69 repeats of a highly

conserved 14 as sequence and a 68 as C-terminal region. This sequence
encodes the GST sequence, the Ag44 polypeptide contg. 16 of the 69

conserved 14 as sequence, the Ag44 polypeptide contg. 16 of the 69

crosest of TCR27. The TCR27 polypeptides of the invention are useful

peptides of TCR27. The TCR27 polypeptides of the invention are useful

crose capable of detecting anti-T.cruzi antibodies; or for blood

sere capable of detecting anti-T.cruzi antibodies; or for blood

creaning. The TCR27 protein has epitopes to which most T cruzi

infected individuals have antibodies. The TCR27 polypeptides will not

creact with serum from patients with leishmaniasis, schistosomissis,

containing and alsees and are hence less likely to cause false
                                       1 AKKYAKK--AEKAYAKKAKAAKE---KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide(s) from the TCR27 protein of Trypanosoma cruzi - a immunoassay reagent for specific diagnosis of Chagas disease, also related nucleic acid and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
329..55
/labels repeat region
/note= "16 of 69 repeat units of 14 amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCR27; Chagas disease; repeat unit; diagnosis; blood screening; recombinant; fusion protein; glutathione-S-transferase.
                                                                                                                                   56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                             Trypanosoma cruzi TCR27 polypeptide, Ag15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 40-41; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                             AAR84568 standard; Protein; 643 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-US03191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0216894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           positives in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIRCHHOFF L V.
OTSU K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kirchhoff LV, Otsu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-344618/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypanosoma cruzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT05332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9525797-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR84568;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Region
                                                                                                                                                                                                                                                                                                      RESULT 13
AAR84568
ID AAR84
XX AAR84
XX DT 09-MA
XX DT 09-MA
XX DT 09-MA
XX TCR27
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The invention provides a method for the diagnosis, prevention and treatment of ulcerative colitis (UC) using histone H1-like antigen, a porin antigen or a Bacteroides antigen as a target antigen. The novel method of diagnosing UC in a subject suspected of having inflammatory bowel disease (IBD) comprises: (1) obtaining a sample from the subject; (2) contacting the sample with a histone H1-like antigen, or perinuclear anti-neutrophil cytoplasmic antibody (DANCA)-reactive fragment, to form a complex of the histone H1-like antigen, or the pANCA-reactive fragment, and antibody to the histone H1-like antigen, and (3) detecting the presence or absence of the complex; where the presence of the complex indicates that the subject has UC. The pANCA-reactive histone H1-like antigen are useful in the antigen and Bacteroides antigen are useful in the antigen and transment of UC. The methods can also be used for identifying agents useful for treating UC. The present sequence represents a human histone H1 isoform H1.5 pANCA-reactive fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
..
                                                                                                                                                                                                                                                                          Ulcerative colitis; histone; H1-like antigen; porin antigen; human; Bacteroides antigen; inflammatory bowel disease; IBD; pANCA; diagnosis; perinuclear anti-neutrophil cytoplasmic antibody; isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 AKPKAKKAGAAKAKKPAGATPKK--AKKAAGAKKAVKKTPKKAKKPAAAGVKKVAKSPKK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAA-----EAKKKAKAEAKKYAKEAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of histone H1, porin or Bacteroides antigens as targets for the diagnosis, prevention and treatment of ulcerative colitis
505 TKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEAA 561
                                                                                                                                                                                                                                         Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20; Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.9%; Score 160.5; DB 20; Length Best Local Similarity 46.8%; Pred. No. 1.9e-06; Matches 51; Conservative 7; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 125-126; 134pp; English
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                                                                                                                    AAY34068 standard; peptide; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US05492.
                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-551215/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cohavy 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 AA;
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                     WO9945955-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1998;
                                                                                                                                                                                                 23-NOV-1999
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                                                                                                                                                            AAY34068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Braun J,
                                                                           RESULT 14
AAY34068
ID AAY3
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Gaps

11;

Query, Match 31.3%; Score 162.5; DB 16; Length 643; Best Local Similarity 44.4%; Pred. No. 5.7e-06; Matches 52; Conservative 18; Mismatches 36; Indels 11;

us-09-816-989a-7.open.rag

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Diagnosing ulcerative colitis or susceptibility, by detecting complex formation between microbial porin antigen and perinuclear anti-neutrophil cytoplasmic autoantibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a method for diagnosing ulcerative colitis in a subject suspected of having inflammatory bowel disease. The method comprises reacting a patient sample with a portin antigen that is immunologically reactive with pANCA (perinuclear anti-neutrophil cytoplasmic antibodies) and detecting formation of a Ag-pANCA complex as indicative of ulcerative colitis. The method is used to diagnose ulcerative colitis or susceptibility to it. Sequences AAYS7362-367 represent pANCA-reactive fragments, derived from human histone HI.S.
                                                                                                                                                  Ulcerative colitis; inflammatory bowel disease; porin antigen; pANCA; perinuclear anti-neutrophil cytoplasmic antibody; human; histone H1; isoform; NANUC-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; Length 158;
                                                                                                                   Human histone H1.5 pANCA-reactive fragment (residues 69-226).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.9%; Score 160.5; DB 2.46.8%; Pred. No. 1.9e-06; Live 7; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Columns 69-70; 49pp; English.
                              AAY57366 standard; peptide; 158 AA
                                                                                                                                                                                                                                                                                                            98US-0041889.
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97US-0837058.
                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA
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Best Local Similarity
Matches 51; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                     Braun J;
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                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                         12-APR-1996;
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                                                                                        13-JUN-2000
                                                                                                                                                                                                                                             US6033864-A.
                                                                                                                                                                                                                                                                            07-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                         AAY57366;
RESULT 15
                AAY57366
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Search completed: March 10, 2003, 12:21:31 Job time : 57.7996 secs

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7;

44; Indels

Conservative

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

March 10, 2003, 12:26:10 ; Search time 32.4241 Seconds
(without alignments)
141.764 Million cell updates/sec

US-09-816-989A-7 519 Title: Perfect score:

1 AKKYAKKAEKAYAKKAKAAK......AKAYKAEAAKAAAKEAAYEA 109 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

188354 segs, 42170167 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2\_6/ptodata/1/pubpaa/USUB\_NEW\_FUB.PEP.\*
/cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
/cgn2\_6/ptodata/1/pubpaa/USO6\_NEW\_PUB.pep.\*
/cgn2\_6/ptodata/1/pubpaa/USO7\_NEW\_PUB.pep.\*
/cgn2\_6/ptodata/1/pubpaa/USO7\_NEW\_PUB.pep.\*
/cgn2\_6/ptodata/1/pubpaa/USO7\_NEW\_PUB.pep.\*
/cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep.\*
/cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep.\*
/cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep.\*
/cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep.\*
/cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep.\*
/cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep.\*
/cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep.\* /ggnZ 6/ptodata/1/pubpaa/US00 PUBCOMB.pep:\* /cgnZ 6/ptodata/1/pubpaa/US10 NEW PUB.pep:\* /cgnZ 6/ptodata/1/pubpaa/US10 PUBCOMB.pep:\* /cgnZ 6/ptodata/1/pubpaa/US60 NEW PUB.pep:\* /cgnZ 6/ptodata/1/pubpaa/US60 NEW PUB.pep:\* Published\_Applications\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 7, Appli	Sequence 6, Appli	ທ	Sequence 4, Appli	Sequence 3, Appli	Sequence 201, App	Sequence 27, Appl	Sequence 24, Appl	Sequence 95, Appl	Sequence 8, Appli	Sequence 23, Appl		Sequence 5, Appli	Sequence 36182, A	Sequence 2, Appli	Sequence 5197, Ap	Sequence 48, Appl	Sequence 11216, A	Sequence 13765, A
ID	US-09-816-989A-7	US-09-816-989A-6	US-09-816-989A-5	US-09-816-989A-4	US-09-816-989A-3	US-10-051-643-201	US-09-820-843A-27	US-09-820-843A-24	US-09-820-843A-95	US-09-820-843A-8	US-09-820-843A-23	US-09-124-280A-3	US-10-184-832-5	US-09-864-761-36182	US-09-816-989A-2	US-09-738-626-5197	US-09-999-724-48	US-09-815-242-11216	US-09-815-242-13765
DB	10	10	10	10	10	σ	σ	σ	σ	σ	σ	10	σ	10	10	σ	0	10	10
* Query Match Length DB	109	86	77	99	26	223	356	309	369	372	352	434	452	617	45	600	218	829	892
Query Match	100.0	60.2	55.7	44.0	34.8	34.3	31.2	29.8	29.6	29.6	27.7	27.7	27.6	26.7	26.6	24.3	23.6	23.6	23.6
Score	519	312.5	. 289	228.5	180.5	178	162	154.5	153.5	153.5	144	144	143.5	138.5	138	126	122.5	122.5	122.5
Result No.	П	7	m	4	2	9	7	80	თ	10	11	12	13	14	15	16	17	18	19

Sequence 7, Appli Sequence 100, App	Sequence 5, Appli	Sequence 10314, A	Seguence 90, Appl	Sequence 46, Appl	Seguence 1, Appli	Sequence 2, Appli	Sequence 559, App	Sequence 1164, Ap	Sequence 9, Appli	Sequence 38, Appl	Sequence 160, App	Sequence 1, Appli	Sequence 7, Appli	Seguence 37061, A	Sequence 268, App	Sequence 5854, Ap	Sequence 5, Appli	Sequence 1271, Ap	Sequence 988, App	Sequence 988, App	Sequence 3538, Ap	Sequence 39625, A	Sequence 245, App	Sequence 245, App
US-10-093-892-7	US-10-093-892-5	0 US-09-815-242-10314	US-09-999-724-90	US-09-999-724-46	US-09-882-774-1	0 US-09-923-304-2	0 US-09-925-302-559	0 US-09-925-300-1164	US-10-093-892-9	0 US-09-765-272-38	0 US-09-765-272-160	0 US-09-816-989A-1	US-09-820-843A-7	0 US-09-864-761-37061	0 US-09-881-752A-268	US-09-738-626-5854	US-09-820-843A-5	0 US-09-925-301-1271	US-09-925-299-988	0 US-09-925-299-988	US-09-738-626-3538	0 US-09-864-761-39625	US-09-978-295A-245	US-09-978-697-245
ο -	ion	Ä	σ,	σ	σ	ī	Ä	Ä	σ	ī	Ä	Ä,	σ	Ä	Ä	σ	σ	Ä	σ	Ä	σ	Ä	σ	0
96	105	890	102	118	619	220	265	300	96	453	641	. 35	203	71	452	365	172	363	606	606	272	87	472	472
22.9	22.7	22.5	22.2	22.2	22.2	21.7	21.7	21.5	21.2	20.4	20.4	20.2	20.1	20.0	19.8	19.6	19.4	19.4	19.4	19.4	19.3	19.2	19.2	19.2
119	118	117	115	115	115	112.5	112.5	111.5	110	106	106	105	104.5	104	103	101.5	100.5	100.5	100.5	100.5	100	99.5	99.5	99.5
20	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
RIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKAEKAYAKKAKAKAKEAKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 519; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.3e-34;
Matches 109; Conservative 0; Mismatches 0;
Sequence 7, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                GENERAL INFORMATION:
APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-816-989A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 7
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1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEA 60 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109 61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109 RESULT 2 US-09-816-989A-6 ; Sequence 6, Application US/09816989A 61 g à g

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Sequence 4, Application US/09816989A

Batent No. US20020115103A1

GENERAL INFORMATION:

APPLICANT: Lis, Doris

APPLICANT: Lis, Doris

TITLE OF INVENTION:

CURRENT APPLICATION AND FOR THERAPEUTIC USE

FILE REPERENCE: 2609/60807-A-PCT-US

CURRENT FILING DATE: 2001-03-23

FRIOR APPLICATION NUMBER: 60/101,693

PRIOR PLING DATE: 1999-09-25

PRIOR PLING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USB AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USB
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKRAEKAYAKKARAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKAEKAYAKKAKAKAKEKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 -KAEAKKYAKAAKAEKKEYAAAEAK------YKAEAAKAAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch
1. Similarity 56.9%; Pred. No. 4.2e-12;
62; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKK-EKAYAKKA-----EAKAAKKA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 34.8%; Score 180.5; DB 1 Similarity 45.9%; Pred. No. 2e-08; 50; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09816989A Patent No. US20020115103A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 7
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 62; Conservi
                                                  RESULT 4
US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-816-989A-3
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               GENERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Lie, Doris

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT APPLICATION NUMBER: 00/101,693

PRIOR APPLICATION NUMBER: PCT/US99/22402

PRIOR FILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PATENTIN VEXSION 3.1

SEQ ID NO 6

SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: US/09/016, 989A
CURRENT APPLICATION NUMBER: US/09/816, 989A
CURRENT APPLICATION NUMBER: 60/101, 693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 5
LENGTH: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 АККҮАККАЕКАУАККАКААКЕККАУАККЕАКАҮКААВАКККАКАЕАККҮАКЕААКАККЕА 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 -KABAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.2%; Score 312.5; DB 10; Length 72.1%; Pred. No. 1.5e-18; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-816-989A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80;
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Sequence 24, Application US/09020843A
Publication No. US20030039963A1
GENERAL INFORMATION:
APPLICANT: COUNCIL Of Scientific and Industrial Research
ITILE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
SEQ ID NO 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,
,
                                      57 KKEAYKAEAKKYAK------AAKAEK----KEYAAAEAKKAEAAKAYKAEAAKA 100
                                                                                                                                                  Gaps
     3 KYAKKAEKAYAKK---AKAAKEKKAYAKKEAKAYKAAEAKKK----AKAEAKKYAKEAAKA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKAEKAYAKKAKAAAKEKKAYAKKEAK-----AYKAAEAKKKAKAEAKKYAKEAA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

OTHER INFORMATION: polyhydroxyalkanoate synthesis protein PhaF

NAME/KEY:
OTHER INFORMATION: gi|9951352

US-09-820-843A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 29.8%; Score 154.5; DB 9; Best Local Similarity 46.9%; Pred. No. 1.2e-05; Matches 53; Conservative 3; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature;
CTHBR INFORMATION: conserved hypothetical protein;
NAME/KEY: misc_feature
HIPORMATION: gl|332751
US-09-820-843A-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 95, Application US/09820843A Publication No. US20030039963A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: T. pallidum
                                                                                                                                                                                                                               101 AAKEAAYEA 109
                                                                                                                                                                                                                                                                                 230 EAERKAQEA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-09-820-843A-95
                                                                                                                                                                                                                                                                                                                                                                                                   US-09-820-843A-24
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LENGTH: 309
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                                                                                                               장, 원
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Sequence 27, Application US/09820843A

Sequence 27, Application US/09820843A

Fublication US/20030039963A1

Sequence 27, Application US/20030039963A1

Sequence 27, Application US/20030039963A1

APPLICANT: Council of Scientific and Industrial Research

TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI

TITLE OF INVENTION: USFPUL AS ANTI-INFECTIVES

FILE REFERENCE: Q63915

CURRENT PAPLICATION UMBER: US/09/820, 843A

CURRENT FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 118

SOFTWARE PATENT OF SEQ ID NOS: 118

SOFTWARE PATENT OF SEQ ID NOS: 118

SOFTWARE PATENT OF SEQ ID NOS: 118

SEQ ID NO 27

TINNENT PATENT OF SEQ ID NOS: 118
                                                                                                                                                                                                                                          Sequence 201, Application US/10051643

Publication No. US20020197265A1

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: System using Mycobacterium Vaccae
TITLE OF INVENTION: System using Mycobacterium Vaccae
TITLE OF INVENTION: System using Mycobacterium Vaccae
CURRENT APPLICATION NUMBER: US/10/051,643

CURRENT PILING DATE: 1098-09-17

PRIOR FILING DATE: 1998-09-17

PRIOR FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 208

SECTIONE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 178; DB 9; Length 223;
Pred. No. 1.3e-07;
6; Mismatches 34; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
     -- 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKK--AEKAYAKKAKAKAKE---KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 356,
                                                       61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                             ----YKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
31.2%; Score 162; DB 9; Length 35:
Best Local Similarity 42.6%; Pred. No. 3.6e-06;
Matches 55; Conservative 13; Mismatches 37; Indels
1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKABEKKKAEAK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
CTHER INFORMATION: tolA protein
NAME/KEY: misc feature
OTHER INFORMATION: gi|9556364
US-09-820-843A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-051-643-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.5%;
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Vibrio cholerae
                                                                                                                                                                                           RESULT 6
US-10-051-643-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 201
LENGTH: 223
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GENERAL INFORMATION:
APPLICANT: POTCO, MASSIMO
TITLE OF INVENTION: VACCINES FOR PREVENTION OF GRAM-
TITLE OF INVENTION: NEGATIVE BACTERIAL INFECTIONS AND ENDOTOXIN RELATED DISEASES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                        ٠<u>.</u>
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                                                                                                                                                                                                                                                                                                              56 -----AKKEAYKAEAKKYAK-----AAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
                                                                                                                                                                                                                                                                                                                                                                     224 Paaktaaakpaakpaakpvakptakpaaktaaakpaakpaakpaakpaakpvaksaaakp 283
                                                                                                                                                                                                                                             1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAK-----AYKAAEAKKKAKAEAKKYAKEAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAEAY 61
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                                                             Length 352;
                                                                                                                        53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTY.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
CAMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 KAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 144; DB 9;
Pred. No. 9.2e-05;
                                       27.7%; bc...
44.0%; Pred. No. >...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Hedman, Gibson & Costigan
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: July 29,1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09124280A Patent No. US20020034520A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Costigan, James V 69 REGISTATION NUMBER: 25,69 REFERENCE/DOCKET NUMBER: 576-TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 302-8989 TELEPHONE: (212) 302-8989 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25,669
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amino acid
                                                    Query Match
Best Local Similarity 44.0
Matches 55, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      circular
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                          105 AAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 AAKPA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
US-09-820-843A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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Publication No. US2003003963A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REPRENCE: Q63315
CURRENT APPLICATION UNMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PALENTIN version 3.0
SEQ ID NO 8
LENGTH: 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-843A-23

Sequence 23, Application US/09820843A

Sequence 23, Application US/09820843A

Sequence 23, Application O. US20030030963A1

GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
TITLE OF INVENTION: USFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION WHORE: US/09/820,843A

CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                        6 KKAEKAYAKKAKAKAKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKA-KKEAYKAE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 KKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA-YKAE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                э
,
                                Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
COTHER INFORMATION: outer membrane integrity protein (tolA)
NAME/KEY: misc_feature
COTHER INFORMATION: gi|1573353
US-09-820-843A-8
                                                                                                                                                                                                                                                                                                                    289 RKEAEEARRKEAEEARRKEAEEARRKEAEEARRKEAEEARRKEAEFEA 336
                                                                                                                                                                                                                                                                                 65 AKKYAKAAKAEKKE---YAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
OTHER INFORMATION: alginate regulatory protein AlgP
NAME/KEY: misc feature
OTHER INFORMATION: gi|9951563
                                                                                           30;
                                DB 9;
                             29.6%; Score 153.5; DB 9; 39.8%; Pred. No. 1.7e-05; cive 26; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 153.5; DB 9
Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 45.3%
nes 48; Conservative
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: H. influenzae
                                                          Local Similarity
hes 43; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-820-843A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 23
LENGTH: 352
                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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Generace 2, Application US/09816989A

Sequence 2, Application US/0981698A

Sequence 2, Application US/0981698A

Sequence 2, Application US/0981698A

GENERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK!

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

TITLE OF INVENTION: ADD FOR THERAPEUTIC USE

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

TITLE OF INVENTION: ADD FOR THERAPEUTIC USE

TITLE OF INVENTION NUMBER: US/09/816,989A

CURRENT FILING DATE: 1998-09-25

PRIOR APPLICATION NUMBER: PCT/US99/22402

PRIOR APPLICATION NUMBER: PCT/US99/22402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 AKSPEKEBAKSPABVKSPEKAKSPAKEBAKSPABAKSPEKAKSPVKEEAKSPAEAKSPVK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 EEAKSPAEVKSPEKAKSPEKAKSPEKAKSPEKEAKSPEKAKSPVKAEAKSPEKAKSP 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 26.7%; Score 138.5; DB 10; Length 617; Best Local Similarity 35.3%; Pred. No. 0.00044; Matches 49; Conservative 17; Mismatches 36; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HELA. SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.6
OTHER INFORMATION: SWISSPROT HIT: BF445754.1, EVALUE 2.00e-32
US-09-864-761-36182
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR PILING DATE: 2000-09-21

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2001-01-29

NUMBER: OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers: 1.1

SEQ ID NO 36182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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US-09-816-989A-2
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APPLICANT: Rain, David R.

APPLICANT: Hancel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: ACONICA-X-1

CURRENT FLING DATE: 2001-05-29

FRIOR FILING DATE: 2000-09-24

FRIOR FILING DATE: 2000-09-27

FRIOR PRILING DATE: 2000-09-27

FRIOR PELING DATE: 2000-09-27

FRIOR PELING DATE: 2000-09-27

FRIOR FILING DATE: 2000-09-27

FRIOR FILING DATE: 2000-09-27

FRIOR FILING DATE: 2001-01-30

FRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                     APPLICANT: Xu et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
FILE REPERENCE: MP12001-056P1NM
CURRENT APPLICATION NUMBER: US/10/184,832
CURRENT PILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/303,250
PRIOR APPLICATION NUMBER: 60/303,250
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PASTESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 AAKEKKAYAKKBAKAYKAAEAKKKAKAKAEAKKYAKEAAKAKKBAYKAEAKKYAKA-AKAEK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 143.5; DB 9;
; Pred. No. 0.00013;
11; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYAAAEAKKAEAAKAYKAEAAKAA----AKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 KAEAKAEA-KAEAKEEWDADSVLGVLLQKLREGYPA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00668
FILING DAFE: 2010-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36182, Application US/09864761
Patent No. US20020048763A1
                                                                                                                   Sequence 5, Application US/10184832
Publication No. US20030022857A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.6%;
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Best Local Similarity 47.41
Matches 46; Conservative
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; ORGANISM: Mus musculus
US-10-184-832-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 452
                                                                                          10-184-832-5
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4; Gaps Query Match 26.6%; Score 138; DB 10; Length 45; Best Local Similarity 76.6%; Pred. No. 3.4e-05; Matches 36; Conservative 0; Mismatches 7; Indels

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Search completed: March 10, 2003, 12:53:45 Job time : 33.5669 secs

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                                                                                                                                   March 10, 2003, 12:15:04 ; Search time 19.3165 Seconds (without alignments) 166.029 Million cell updates/sec
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                                                                                                                                                                                                                                                                                1 AKKYAKKAEKAYAKKAKAK...........AKAYKAEAAKAAAKEAAYEA 109
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(c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-167-641C-64
US-08-460-971A-64
US-08-460-971A-64
US-09-095-855-201
US-09-015-855-201
US-09-115-746-8
US-09-115-746-8
US-09-041-889-40
US-09-041-889-40
US-09-115-746-10
US-09-115-746-10
US-09-115-746-2
US-09-115-746-2
US-09-115-746-2
US-09-041-889-4
US-09-041-889-4
US-09-041-889-3
US-08-837-058-3
US-08-837-058-3
US-08-837-058-3
US-08-93-329-5
US-08-93-329-5
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US-08-167-641C-62
US-08-460-971A-62
US-08-462-040-62
US-09-041-889-1
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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519
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Maximum DB
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                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
No.
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	ALIGNMENTS					
Seguence 8, App	US-08-762-106-8	N	216	23.8	123.5	45
Sequence 23, Appl	US-08-894-017-23	m	1561	24.0	124.5	44
Sequence 6, Appli	US-08-993-008A-6	4	26	24.4	126.5	43
Sequence 51, Appl	US-09-256-976-51	4	263	24.7	128	42
Sequence 51, Appl	US-08-993-674A-51	4,	263	24.7	128	41
51,	US-08-834-306-51	ო	263	24.7	128	40
Sequence 51, Appl	US-08-557-309B-51	~	263	24.7	128	39
H	US-08-929-414-1	~	262	24.7	128	38
Sequence 1, App	US-08-403-379A-1	-	262	24.7	128	37
Sequence 2, Appli	US-08-837-058-2	m	220	25.0	129.5	36
7	US-09-041-889-2	ო	220	25.0	129.5	35
13,	US-08-837-058-13	e	147	25.0	129.5	34
Sequence 13, Ap	US-09-041-889-13	ᠬ	147	25.0	129.5	33
	US-08-837-058-14	ო	113	25.0	129.5	32
	US-09-041-889-14	ო	113	25.0	129.5	31
Sequence 2, App	US-08-293-284A-2	~	433	25.6	133	30
Sequence 2, Appli	US-08-346-849-2	ч	433	25.6	133	53
Sequence 1, Appl:	US-08-837-058-1	ო	212	25.7	133.5	28

Sequence 64, Application US/08460890A

Patent No. 5994109

GENERAL INFORMATION:

APPLICANT: Woo, Savio L.C.

APPLICANT: Smith, Louis C.

APPLICANT: Gittano, Richard J.

APPLICANT: Gottchalk, Stephen

TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND

TITLE OF INVENTION: METHODS OF USE

NUMBER OF SEQUENCES:

ADDRESSEB: Lyon & Lyon

ADDRESSEB: Lyon & Lyon ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-206
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage US-08-460-890A-64

COMPUTER: IEM Compatible
OPERATING SYSTEM: IEM P.C. DOS 5.0
OPERATING SYSTEM: IEM P.C. DOS 5.0
SOFTWARE: FastERG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: Une 5, 1995
CLASSIFICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY AGENT INFORMATION:

NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 21 TELECOMMUNICATION INFORMATION:

(213) 489-1600

TELEPHONE: (213) 489-160 TELEFAX: (213) 955-0440 TELEX: 67-3510 INFORMATION FOR SEQ ID NO: 6

LENGTH: 100 amino acids TYPE: amino acid STRANDEDNESS: single

<u>ب</u>

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10 КАҮАК-ХАКААКЕККАУАККЕАКАУКААБАКККАКАБАККУАКБААКАККЕАУКАБАККУ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: NETHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: Gailfornia
CONTRY: Los Angeles
STREET: Gailfornia
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER READABLE FORM:
MEDIUM TYPE: JONE STORAGE
COMPUTER: DISK COMPACTION DATA:
APPLICATION NUMBER: US/08/460,971A
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 19, 1993
APPLICATION NUMBER: PCT/US93
ATTORNEY AGENT POLICATION
NAME: WATHING DATE: MARCH 19, 1993
ATTORNEY AGENT POLICATION
NAME: WATHING DATE: MARCH 19, 1993
ATTORNEY AGENT POLICATION
NAME: WATHING DATE: MARCH 19, 1993
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۳
                                                     Length 100;
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US-08-460-971A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.6%; Score 179.5; DB 4; Length 100;
                                                                                                     Indels
                                               Score 179.5; DB 3;
Pred. No. 7.5e-09;
8; Mismatches 33;
                                                                                                                                                                                                                                                          69 АКА-АКАЕККЕУАААБАККАЕААКАҮКАЕААКАААКЕАА 106
                                                                                                                                                                                                                                                                                                          60 akakakakakakakakakakakakakakakaka 98
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 64, Application US/08460971A
Patent No. 6150168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : (213) 489-1600
; TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION
                                                     34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
                                                  Query Match
Best Local Similarity 55.6'
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
linear
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
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  US-08-167-641C-64
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                                                                                                                                                                                                                                                                                  10 KAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKY 68
                                                                                                                                                                                                                                                                                                                  DB 2; Length 100;
                                                                       OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-460-890A-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gritchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES:
ADDRESSEE: Lyon & Lyon
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                               33; Indels
                                                                                                                                                                                                                                                                                                                                                                                       69 AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 34.6%; Score 179.5; DB 2 Best Local Similarity 55.6%; Pred. No. 7.5e-09; Matches 55; Conservative 8; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 206/012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ 10
TELEFAX: (213) 985-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ 1D NO: 64:
SEQUENCE CHARACTERISTICS:
FUNCTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 64, Application US/08167641C Patent No. 6033884 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-167-641C-64
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Sequence 201, Application US/09095855; Patent No. 6160093; GENERAL INFORMATION:
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TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-09-095-855-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98121
                                                                                                                                                                                                                                             US-09-095-855-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                  RESULT 5
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                           3; Gaps
                                                                       10 KAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKY 68
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gristiano, Richard J.
APPLICANT: MINISTIANO OF USE
NUMBER OF ROUTENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
                        33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                   69 AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                              Best Local Similarity 55.6%; Pred. No. 7.5e-09;
Matches 55; Conservative 0; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 6.5" ON 5.0
SOFTWARE: 1BM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: 187 S.0.0
FILING DATE: 187 S.0.0
FILING DATE: 1995
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 20, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
FILING DATE: MARCH 33, 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/078
TELECOMMUNICATION INFORMATION:
TELEPAX: (213) 955-0440
TELEFAX: (67-3510
TELEFAX: (67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                 Sequence 64, Application US/08462040
Patent No. 6177554
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RY: U.S.A.
90071-2066
                                                                                                                                                                                                                                                                                                                US-08-462-040-64
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APPLICANT: Viser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 АККААККАРАККАЛАККААРАККАРАККА-АТКААРАККАТААККАРАККАТААККАР 170
10 KAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKY 68
                                  34; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKK--AEKAYAKKAKAAKE---KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 34.3%; Score 178; DB 4; Length 223; Best Local Similarity 54.5%; Pred. No. 2.2e-08; Matches 60; Conservative 6; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                  AKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                     60 AKAKAKAKAKAKAKAKAKAKAKAKAKAKAKA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11000.1002c3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-UNN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REGISTRATION NUMBER: 11000.10
TELECOMMUNICATION INFORMATION:
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904136
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TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08216894
| Patent No. 5876734
| GENERAL INFORMATION:
| APPLICANT: Kirchhoff, Louis V. APPLICANT: Otsu, Keiko
| TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
| TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
| NUMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Foley & Lardner | STREET: 3000 K Street, N.W., Suite 500 |
| CITY: Washington, D.C.
                                                        Sequence 201, Application US/09205426

Patent No. 6406704

GRUERAL INFORMATION:
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
FILE REFERENCE: 11000.100.204
CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT APPLICATION NUMBER: 09/095,855
EARLIER APPLICATION NUMBER: 09/095,855
EARLIER FILING DATE: 1998-06-11
EARLIER FILING DATE: 1997-06-12
EARLIER FILING DATE: 1996-08-29

NUMBER OF SEQ ID NOS: 208

SOFTWARRE: PastSEQ for Windows Version 3.0

LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.3%; Score 178; DB 4; Length 223; Best Local Similarity 54.5%; Pred. No. 2.2e-08; Matches 60; Conservative 6; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 AKKEAYKAEAKKYAKAAKAEKKEYA--AAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MRR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 93.768
REFERENCE/DOCKET NUMBER: 85.326/102/DRLO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-205-426-201
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(202) 672-5399
                    RESULT 6
US-09-205-426-201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-216-894-8
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                                                                                                                                                                                                                                                                                                                                                                                         505 TKVAEAEKQKAAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEAA 561
                                                                                                                                                                                  Length 643;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09115746

Retent No. 6228601

GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardher
                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                31.3%; Score 162.5; DB 2;
ilarity 44.4%; Pred. No. 1.3e-06;
Conservative 18; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
FILING DATE:
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.3%; Score 162.5; DB 4; ilarity 44.4%; Pred. No. 1.3e-06; Conservative 18; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85326/102/DRLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: FOLEY & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 8532
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIF: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHRARACTERISTICS:
LENGTH: 643 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 643 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (202) 672-5399
                                                                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-216-894-8
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                                                                                                                                                                           Query Match
Best Local Similarity
Matches 52; Conserv
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Matches 52; Conserv
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                              FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC pANCA antigens
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
ADDRESSE: Campbell & Flores LLP
STRET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosis, Prevention and Treatment of
Ulcerative Colitis, and Clinical Subtypes Thereof, Using
Microbial UC pANCA antigens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAA-----EAKKKAKAKAEAKKYAKEAAK 55
57 KK--EAYKAEAKKYAKAAKAEKKEYA----AAEAKKAEAAKAYK-AEAAKAAAKEAA 106
                            505 TKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEAA 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/041,889
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.9%; Score 160.5; DB 3
46.8%; Pred. No. 4.6e-07;
tive 7; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A.
REGIGSTRATION UNUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECHOMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/09041889
Patent No. 6033864
GBNEALINFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Previ
                                                                                                                                                     Sequence 40, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 158 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 46.8
Matches 51; Conservative
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US-09-041-889-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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119 AKPKAKKAGAAKAKKPAGATPKK--AKKAAGAKKAVKKTPKKAKKPAAAGVKKVAKSPKK 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 AKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR.1994
ATTORNEY/AGENT INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               us-08-216-894-10
; Sequence 10, Application US/08216894
; Patent No. 5876734
; GENERAL INFORMATION:
; APPLICANT: Kirchhoff, Louis V.
; APPLICANT: Oresu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAG;
; TITLE OF INVENTION: AUTH TRYPANOSOMA CRUZI,
; NAMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READANIT:
MEDITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Cambell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                              COUNTRA.
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Conservative
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Matches 51; Conservative 18; Mismatches 36; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-115-746-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 KK--EAYKAEAKKYAKAAKAEKKEYA----AAEAKKAEAAKAYK-AEAAKAAKEA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 TKVAEABKÇKAABEATKVAEABKÇKAABATKVAEABKÇKAABATKVABABEKÇKAABA 430
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Patent No. 6228601
GENERAL INFORMATION:
FAPPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 3000 & Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                          Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 158.5; DB 4; Length 472; Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                     30.5%; Score 158.5; DB 2; Length 44.0%; Pred. No. 2e-06; Live 18; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 472 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 44.0 Matches 51; Conservative
                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-216-894-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match?
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-115-746-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-115-746-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
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                                                   1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAKAEAKKYA----KEAAKA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYA----KEAAKA 56
                                                                                                                                                                                            375 TKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEA 430
                                                                                                                                                            57 KK--BAYKABAKKYAKAAKABKKBYA----AABAKKABAAKAYK-ABAAKAAAKBA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 KK--EAYKAEAKKYAKAAKAEKKEYA----AAEAKKAEAAKAYK-AEAAKAAKEA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491 TKVAEAEKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAAEA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Orsu, Kölko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: POLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09115746
Patent No. 6228601
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILLING DATE: 24-MAR.199
ATTORNEY/AGENT INFORMAR.199
ATTORNEY/AGENT INFORMAR.199
REFERENCE/DOCKET NUMBER: 29.768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.5%; Score 158.5; DB 2
44.0%; Pred. No. 2.4e-06;
tive 18; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                         US-08-216-894-2
; Sequence 2, Application US/08216894
; Patent No. 5876734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 0, 2099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 51; Conserva
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NUMBER OF SEQUENCES: 10

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Search completed: March 10, 2003, 12:30:04 Job time : 20.3165 secs
                                                                                                                                                                                                                                              : 218 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                             LOCATION: 1.218
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide LOCATION: 1..218
                                                                                                                                                                                                                                                                 TYPE: amir
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                          US-09-041-889-4
                                                                                                                                                                                                                                                LENGTH:
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APPLICANT: Braun, Jonathan
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAKAEAKKYA----KEAAKA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     491 TKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 KK--EAYKAEAKKYAKAAKAEKKEYA----AAEAKKAEAAKAYK-AEAAKAAKEA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 30.5%; Score 158.5; DB 4; Length EBest Local Similarity 44.0%; Pred. No. 2.4e-06; Matches 51; Conservative 18; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIF: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                           APPLICALION
FILING DATE:
ATORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET UNBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09041889 Patent No. 6033864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 564 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-115-746-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-041-889-4
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108 KKAASGEAKPKAKKAGAAKAKKPAGAAKKPKKATGAATPKKSAKKTPKKAKKPAAA--G 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 AYKAEAKKYAKAAKAEK--KEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "product = Human Histone
H1-S-4"
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/837,058
FILIND DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET: 31,815
REFERENCE/DOCKET: 11-APR-1997
TELECOMMUNICATION INFORMATION:
TELECHONE: (619) 535-9001
TELEPAK: (619) 535-9001
TELEPAK: (619) 535-9001
SEQUENCE CHARACTERISTICS:
```

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